



QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGAGAGATTGAGACCCGTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGAGAGATTGAGACCCGTTCCGCGCAC 180  
QY 181 TTCTGTGACCTGGCGCTGAGCTGACGTCAGCCCAAGGCTGACCCAGCAACGCTTCAAC 240  
DB 181 TTCTGTGACCTGGCGCTGAGCTGACGTCAGCCCAAGGCTGACCCAGCAACGCTTCAAC 240  
QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTGTGGCATTTCTT 300  
QY 301 GTCCTTGGGGCGCTGCTGTGCTGAGTGTCAAGTGTCAAGAAATGAGAGCTTTGGTGGGA 360  
DB 301 GTCCTTGGGGCGCTGCTGTGCTGAGTGTCAAGTGTCAAGAAATGAGAGCTTTGGTGGGA 360  
QY 361 CAAGTGCAGAGATTGGATGGTGGCTTACCTGAGAGACGCTGTGGTGAATGACACAGC 420  
DB 361 CAAGTGCAGAGATTGGATGGTGGCTTACCTGAGAGACGCTGTGGTGAATGACACAGC 420  
QY 421 AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGAGAGGGGCGCTGAGAGAGCAGCG 480  
DB 421 AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGAGAGGGGCGCTGAGAGAGCAGCG 480  
QY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGAGACAGTGTGACCGGGGCGCTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGAGACAGTGTGACCGGGGCGCTGGCACTG 540  
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAGTG 581  
DB 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAGTG 581

## RESULT 2

US-09-925-674A-6  
; Sequence 6, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-925-674A-6

Query Match 90.6%; Score 526.6; DB 9; Length 583;  
Best Local Similarity 94.1%; Pred. No. 16-142;  
Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTTCAACCCCAAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGGACCCCAAGCTTCAACCCCAAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AAGCTGAGGACAGAAAGGTTATGTCGTGAGCTGGGCGCTGGGAGAGGCCAGCCGCGAC 120  
DB 61 AAGCTGAGGACAGAAAGGTTATGTCGTGAGCTGGGCGCTGGGAGAGGCCAGCCAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCGTGTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCGTGTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 180

DB 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGAGATGATTGAGACCCGCTTCCGCGCAC 180  
QY 181 TTCTGTGACCTGGCGCTGAGCTGACGTCAGCCCAAGGCTGACCCAGCAACGCTTCAAC 240  
DB 181 TTCTGTGACCTGGCGCTGAGCTGACGTCAGCCCAAGGCTGACCCAGCAACGCTTCAAC 240  
QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTGTGGCATTTCTT 300  
QY 301 GTCCTTGGGGCGCTGCTGTGCTGAGTGTCAAGTGTCAAGAAATGAGAGCTTTGGTGGGA 360  
DB 301 GTCCTTGGGGCGCTGCTGTGCTGAGTGTCAAGTGTCAAGAAATGAGAGCTTTGGTGGGA 360  
QY 361 CAAGTGCAGAGATTGGATGGTGGCTTACCTGAGAGACGCTGTGGTGAATGACACAGC 420  
DB 361 CAAGTGCAGAGATTGGATGGTGGCTTACCTGAGAGACGCTGTGGTGAATGACACAGC 420  
QY 421 AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGAGAGGGGCGCTGAGAGAGCAGCG 480  
DB 421 AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGAGAGGGGCGCTGAGAGAGCAGCG 480  
QY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGAGACAGTGTGACCGGGGCGCTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGAGACAGTGTGACCGGGGCGCTGGCACTG 540  
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAGTG 581  
DB 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAGTG 581

## RESULT 3

US-09-809-391-130  
; Sequence 130, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 1864  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1648)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-809-391-130

Query Match 64.6%; Score 375.6; DB 10; Length 1864;  
Best Local Similarity 91.7%; Pred. No. 6-9e-9;  
Matches 396; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTTCAACCCCAAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGGACCCCAAGCTTCAACCCCAAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 70  
QY 61 AAGCTGAGGACAGAAAGGTTATGTCGTGAGCTGGGCGCTGGGAGAGGCCAGCCGCGAC 120  
DB 71 AAGCTGAGGACAGAAAGGTTATGTCGTGAGCTGGGCGCTGGGAGAGGCCAGCTGAC 130  
QY 121 CCGCTGACCAAGCCATGCGGCGTGTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCGTGTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 180  
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DB 181 TTCTGTGACCTGGCGCTGAGCTGACGTCAGCCCAAGGCTGACCCAGCAACGCTTCAAC 250

QY 241 CAGGTTCCGACGACTTTTCCAGGGGGCCCTAAGTGGGGCGTCTTGTGGCAATCTT 300  
 Db 251 CAGGTTCCGACGACTTTTCCAGGGGGCCCTAAGTGGGGCGTCTTGTGGCAATCTT 310  
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 Db 311 GCTTTGGGGGCTGACCTGTGTGTGAGTGTCAAGAAATGAGCACTGTGGGA 370  
 QY 361 CAAGTGAGAGTGTGATGTGTGCTTACCTGAGACACGCTGTGCTGATGATCCAGC 420  
 Db 371 CAAGTGAGAGTGTGATGTGTGCTTACCTGAGACACGCTGTGCTGATGATCCAGC 430  
 QY 421 AGTGGGGGCTGG 432  
 Db 431 AGTGGGGGCTGG 442  
 RESULT 4  
 US-09-882-171-130  
 ; Sequence 130, Application US/09882171  
 ; Publication No. US20030175858A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P2  
 ; CURRENT APPLICATION NUMBER: US/09/882,171  
 ; CURRENT FILING DATE: 2001-06-18  
 ; PRIOR APPLICATION NUMBER: 09/809,391  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 09/149,476  
 ; PRIOR FILING DATE: 1998-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493  
 ; PRIOR FILING DATE: 1998-03-06  
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PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/057,650  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: 60/056,884  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/057,669

PRIOR FILING DATE: 1997-09-05  
Query Match 64.6%; Score 375.6; DB 10; Length 1864;  
Best Local Similarity 91.7%; Pred. No. 6.9e-99;  
Matches 396; Conservative 1; Mismatches 35; Indels 0; Gaps 0;  
QY 1 ATGGGACCCCAAGCTCAACCCAGACACAGAGGCTGTAGTGTGACTTTGTAGGCTAT 60  
DB 11 ATGGGACCCCAAGCTCAACCCAGACACAGAGGCTGTAGTGTGACTTTGTAGGCTAT 70  
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGCGCTGGGGAAGCCCGCCGAC 120  
DB 71 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGCGCTGGGGAAGCCCGCCGAC 130  
QY 121 CCGCTGACCAAGCATCGGGGCTGTGAGACGAGTGTGAGACCCGTTCCGCGCAC 180  
DB 131 CCGCTGACCAAGCATCGGGGCTGTGAGACGAGTGTGAGACCCGTTCCGCGCAC 190  
QY 181 TTCTGTGACTGCGCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCAC 240  
DB 191 TTCTGTGACTGCGCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCAC 250  
QY 241 CAGGTTTCCGACGAATTTCGAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTCTT 300  
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QY 301 GTCTTTGGGCGCTGCGCTGTGTGCTGAGCTGCAACAAAGAAATGGAGCCTTTGGTGG 360  
DB 311 GTCTTTGGGCGCTGCGCTGTGTGCTGAGCTGCAACAAAGAAATGGAGCCTTTGGTGG 370  
QY 361 CAAGTGACAGATTGGATGTGGCTTACCTGAGACACCTGTGCTGACTGTGATCCACAGC 420  
DB 371 CAAGTGACAGATTGGATGTGGCTTACCTGAGACACCTGTGCTGACTGTGATCCACAGC 430  
QY 421 AGTGGGGGCTGG 432  
DB 431 AGTGGGGGCTGG 442  
RESULT 5  
US-10-029-386-10549  
Sequence 10549, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
FILE REFERENCE: AROMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 10549  
LENGTH: 578  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR14.3  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2  
OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALU0 0.00e+00  
OTHER INFORMATION: NT HIT: g1475151, EVALU0 0.00e+00  
OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALU0 2.00e-72  
US-10-029-386-10549  
Query Match 64.6%; Score 375.4; DB 14; Length 578;  
Best Local Similarity 91.7%; Pred. No. 6.7e-99;



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Db	122	CCGCTGCACCAAGCCATGCGGGGCTGTGGAGAGTTGTGAGACCCGCTTCCGGGGCAC	181
OY	181	TTCTCTGACTTGGCCGCTCAGCTACAGCTGACCCGAGCTCAGCCACGACGCTTACCC	240
Db	182	TTCTCTGACTTGGCGGCTCAGCTGATGTGACCCGAGCTCAGCCCAACAGCTTCAAC	241
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Db	242	CAGGTTTCGAGTAACCTTTCGAAGGGGCGCTTAACTGAGGGCGGCTTGTAGACTTCTT	301
OY	301	GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACTTTGTGTGGA	360
Db	302	GTCTTTGGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAAGAGATGTGAACCACTGTGTGGGA	361
OY	361	CAAGTGACAGAGATTGATGTGTGGCTAAGCTGGAGACAGGCTGTGGCTGATGTGCACAGC	420
Db	362	CAAGTGACAGAGATGTGTGGCTAAGCTGGAGACGACGCTGTGACTGATTCAGATCCACAGC	421
OY	421	AGTGGGGGCTGG 432	
Db	422	AGTGGGGGCTGG 433	

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/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting Cytosine Methylation
/ TITLE OF INVENTION: Cytosine methylation
/ FILE REFERENCE: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ CURRENT FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 201
/ LENGTH: 6049
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201

Query Match      38.2%   Score 221.8;  DB 14;  Length 6049;
Best Local Similarity 69.5%;  Pred. No. 3e-54;
Matches 301;  Conservative 0;  Mismatches 133;  Indels 0;  Gaps 0;

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QY 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGGCCACGCCCGAC 120

DB 5061 AAGTTGAGGTGAAAGGCTTATGTTGTGTGAGTGGTTTCGGGGAGGGCTTTAGTACTGAT 5120

QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACAGTTGAGACCCGTTTCCGCCGCAC 180

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RESULT 8
US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 1002529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

Query Match 33.4%; Score 194.2; DB 14; Length 6049;
Best Local Similarity 66.2%; Pred. No. 3e-46;
Matches 280; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 1 AAGGAGACCCCAAGCTTCAACCCCAAGACGAGGAGCTTGAAGCTTTAGAGCTAT 60
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Db 809 CAATCTCCGATTAACCTTTTCAAAAAAACCACCTAAACCCGCTTAATACCTTCTT 750
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Qy 361 CAGTGCAGGATTTGATGGTGGCTTACCTCGAGACACGTCGTGCTGATCGATCCACAGC 420
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Qy 421 AGT 423
Db 629 AAT 627

RESULT 9
US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUATE 5.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUATE 3.00e-11
; OTHER INFORMATION: NT HIT: g14574571, EVALUATE 9.00e-80
US-10-029-386-27084

Query Match 25.5%; Score 148.4; DB 14; Length 151;
Best Local Similarity 99.3%; Pred. No. 3.3e-33;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 432 GCGGAGTTCAAGCTCTATACGGGACGGGCGCTGAGAGGACGCGCTTGGCGGGA 491
Db 1 GCGGAGTTCAAGCTCTATACGGGACGGGCGCTGAGAGGCGCGCTTGGCGGGA 60
Qy 492 GGGGACCTGGGATCATGATGAGACAGTCTGACGCGGGGCGCTGGCATCTGGGGCGCTTGT 551
Db 61 GGGGACCTGGGATCATGATGAGACAGTCTGACGCGGGGCGCTGGCATCTGGGGCGCTTGT 120
Qy 552 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 121 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 150

RESULT 10
US-10-029-386-13384
; Sequence 13384, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
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NUMBER OF SEQ ID NOS: 3428
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13384
LENGTH: 590
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR14.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALU 2.00e-10
OTHER INFORMATION: NT HIT: G14751151, EVALU 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALU 1.00e-119
US-10-029-386-13384

Query Match      25.5%; Score 148.4; DB 14; Length 590;
Best Local Similarity 99.3%; Pred. No. 4e-33;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 432 GCGGAGTTCAAGCTCTATACGGGAGCGGCGCTTGAGAGGACCGCGTTGCGGGA 491
Db 25 GCGGAGTTCAAGCTCTATACGGGAGCGGCGCTTGAGAGGACCGCGTTGCGGGA 84
Qy 492 GGGAACTGGGCACTAGTAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCT 551
Db 85 GGGAACTGGGCACTAGTAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCT 144
Qy 552 AACTGATGGGCGCTTTTGTGCTAGCAAGTG 581
Db 145 AACTGATGGGCGCTTTTGTGCTAGCAAGTG 174

RESULT 11
US-09-864-761-17690
Sequence 17690, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecmica-X-1
CURRENT FILING DATE: US/09/864,761
PRIOR APPLICATION NUMBER: 2001-05-23
PRIOR FILING DATE: US 60/180,312
PRIOR APPLICATION NUMBER: 2000-02-04
PRIOR FILING DATE: US 60/207,456
PRIOR APPLICATION NUMBER: 2000-05-26
PRIOR FILING DATE: US 09/632,366
PRIOR APPLICATION NUMBER: 2000-08-01
PRIOR FILING DATE: GB 24263.6
PRIOR APPLICATION NUMBER: 2000-10-04
PRIOR FILING DATE: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17690
LENGTH: 150
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049829.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: NT HIT: D87461.1, EVALU 2.00e-79
OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALU 8.00e-70
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALU 3.00e-11
US-09-864-761-17690

Query Match      25.4%; Score 147.4; DB 9; Length 150;
Best Local Similarity 99.3%; Pred. No. 6.3e-33;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 433 GCGGAGTTCAAGCTCTATACGGGAGCGGCGCTTGAGAGGACCGCGTTGCGGAG 492
Db 1 GCGGAGTTCAAGCTCTATACGGGAGCGGCGCTTGAGAGGACCGCGTTGCGGAG 60
Qy 493 GGGAACTGGGCACTAGTAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCTA 552
Db 61 GGGAACTGGGCACTAGTAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCTA 120
Qy 553 AACTGATGGGCGCTTTTGTGCTAGCAAGTG 581
Db 121 AACTGATGGGCGCTTTTGTGCTAGCAAGTG 149

RESULT 12
US-10-402-017-5
Sequence 5, Application US/10402017
Publication No. US2003021987A1
GENERAL INFORMATION:
APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
FILE REFERENCE: Case 1/1314
CURRENT FILING DATE: US/10/402,017
PRIOR FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/369,307
PRIOR APPLICATION NUMBER: April 2, 2002
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 540
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del26-83)
US-10-402-017-5

Query Match      24.3%; Score 141.2; DB 15; Length 540;
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Db	478	CTTACCGAAAACATGATGACAGCTGAGAGCCGGAAAGGCCAGAGCGCTTACACCGCTGG	537
Qy	508	GTGAGGACAGTGTCTGACGGGGGCGG	532
Db	538	TTCTCTGACGGGCAATGACTGTGGCTGG	562

Db 557 AGAAGCCTTCAACCGTGTCTCTACGGGATGACTGTGGCG 601

Search completed: March 3, 2004, 19:53:48

Job time : 330 secs

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RESULT 15
US-10-169-223-13
# Sequence 13, Application US/10169223
# Publication No. US20030152946a1
# GENERAL INFORMATION:
# APPLICANT: SHIMIZU, Shigeomi
# APPLICANT: TSUJIMOTO, Yoshhide
# TITLE OF INVENTION: Bk4-Fused Polypeptides
# FILE REFERENCE: 1422-0537P
# CURRENT APPLICATION NUMBER: US/10/169,223
# CURRENT FILING DATE: 2002-11-05
# PRIOR APPLICATION NUMBER: JP 11-371449
# PRIOR FILING DATE: 1999-12-27
# PRIOR APPLICATION NUMBER: PCT/JP00/09274
# PRIOR FILING DATE: 2000-12-26
# NUMBER OF SEQ ID NOS: 35
# SOFTWARE: PatentIn version 3.1
# SEQ ID NO 13
# LENGTH: 636
# TYPE: DNA
# ORGANISM: Artificial Sequence
# OTHER INFORMATION: Synthesized DNA for mutant bcl-xL
# FEATURE:
# NAME/KEY: CDS
# LOCATION: (1)..(636)
# OTHER INFORMATION:
US-10-169-223-13

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 Oy 188 AACTGGCCGCTCAGCTACACGTGACCCCAAGCTCAGCCCAAGCAACGCTTACCCAGATT 247  
 Db 257 ACCTGACATCCGAGCTCCACATCAACCCCAAGGAGACACATATCAGACTTTTGAACAAGTAG 316  
 Oy 248 CCGAAGACCTTTTCCAGGGGGCCCTTAATCTGGGGCCGTCCTTGTGGCATCTTTGTCTTGG 307  
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 Oy 368 AGGATTGGATGGTGGGCTTACCTTGGAGACACGTTGGCTACTTGGATTCACACGAGTGGGG 427  
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 Oy 428 GCTGGGCGGAGTTCACAGCTTATACGGGGGACGGGCGCCTTGAGAGAGGACAGCGCGTCTGC 487  
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us-09-508-745-3.rge

Bertog 1.0  
09/508745 Page 1  
Seq 105 374

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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Yes	Count	Count
	Watch	Watch
	Month	Month
	IN	IN
		Description

(without alignments)

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Pred. No. is the number of results predicted by chance to have a

no motivation

JOURNAL Oncogene 13 (4), 665-675 (1996)  
MEDLINE 96358615  
PUBMED 8761287  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Gibson, L., Holmgren, S. E., Huang, D. C. S., Bernard, O., Adams, J. M. and Cory, S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia  
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Best Local Similarity 100.0%; Pred. No. 5.3e-131;  
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DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.  
ACCESSION AF030769  
VERSION AF030769.1 GI:2623249  
KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)  
REFERENCE  
1 (bases 1 to 3476)  
Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.  
AUTHORS Ross, A. J., Maymire, R. G., Moss, J. E., Parlow, A. F., Russell, L. D. and MacGregor, G. R.  
TITLE Bcl-w is required for testis homeostasis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3476)  
AUTHORS Rose, A. J. and MacGregor, G. R.  
TITLE Direct Submission  
JOURNAL Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA  
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ORIGIN  
Query Match 100.0%; Score 581; DB 10; Length 3476;  
Best Local Similarity 100.0%; Pred. No. 4.3e-131;  
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGGACCCCGAGCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 179 ATGGGACCCCGAGCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 238  
QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCCGCAGC 120



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Qy	181	TTCTGTGACCTGGCGGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAACGCTTCACC	240
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Qy	241	CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTAACCTGGGGCCGTCTTGTGGCAATCTTT	300
Db	419	CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTAACCTGGGGCCGTCTTGTGGCAATCTTT	478
Qy	301	GTCCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCCAAAGAAATGGAAGCTTTTGTGGGA	360
Db	479	GTCCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCCAAAGAAATGGAAGCTTTTGTGGGA	538
Qy	361	CAAGTGCAGAGATTGGATGTGGCTTAACCTGGAGACACGTCGTGGCTACGTGATCCACAGC	420
Db	539	CAAGTGCAGAGATTGGATGTGGCTTAACCTGGAGACACGTCGTGGCTACGTGATCCACAGC	598
Qy	421	AGTGGGGGCTGGGCGGAGTTCAAGCTCTAATACGGGGACGGGGCCCTGGAGGAGGACGG	480
Db	599	AGTGGGGGCTGGGCGGAGTTCAAGCTCTAATACGGGGACGGGGCCCTGGAGGAGGACGG	658
Qy	481	CGTCTGCGGGAGAGGGAACTGGGCAATCAGTGAGAGACAGTGTCTGACGGGGGCGTGGACCTG	540
Db	659	CGTCTGCGGGAGAGGGAACTGGGCAATCAGTGAGAGACAGTGTCTGACGGGGGCGTGGACCTG	718
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RESULT 3
AF096291
LOCUS AF096291 582 bp mRNA linear ROD 28-FEB-2000
DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION AF096291
VERSION AF096291.1 GI:3747129
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 582)
AUTHORS Hammer,S., Skogjosa,Y. and Lindholm,D.
TITLE Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
JOURNAL Neurosciences 91 (2), 673-684 (1999)
MEDLINE 99292146
REFERENCE 2 (bases 1 to 582)
AUTHORS Hammer,S., Skogjosa,Y. and Lindholm,D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES
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Query Match	97.2%	Score	565	DB	10	Length	582
Best Local Similarity	98.3%	Pred.	No.	4,28	127		
Matches	571	Conservative	0	Mismatches	10	Indels	0

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Db	1	ATGGCGA	CCCCAGCCTCA	CCCCAGACAC	AGGCGCTCTA	GTGGCTGACTTTGT	TGAGCTAT	60		
QY	61	AAGCTGA	GGCGAGAGGGTTAT	TGTGTGTG	AGCTGAGCTGGCCCTGGG	GAAGGCCAGCCGCGC	AG	120		
Db	61	AAGCTGA	GGCGAGAGGGTTAT	TGTGTGTG	AGCTGAGCTGGCCCTGGG	GAAGGCCAGCCAGCCG	AG	120		
QY	121	CCGCTGA	CACCAAGCCATG	CGGGGCTGTG	AGACGAGT	TTTGAGACCCGTTTCCG	CGCAC	180		
Db	121	CCGCTGA	CACCAAGCCATG	CGGGGCTGTG	AGACGAGT	TTTGAGACCCGCTTCCG	CGCAC	180		
QY	181	TTCTCTG	ACCTGGGCGCGCTCA	AGTCA	CACTGAC	CCCCAGGCTTA	AGCCACGACCA	CGTTAC	240	
Db	181	TTCTCTG	ACCTGGGCGCGCTCA	AGTCA	CACTGAC	CCCCAGGCTTA	AGCCACGACCA	CGTTAC	240	
QY	241	CAGGTTTCCG	ACGAACTTTTCA	AGGGGGGCGCCTTA	CTGAGG	GGCGCTGTGTG	GGCAATTC	300		
Db	241	CAGGTTTCCG	ACGAACTTTTCA	AGGGGGGCGCCTTA	CTGAGG	GGCGCTGTGTG	GGCAATTC	300		
QY	301	GTCCTTTG	GGGGCTGCGCTGTGTG	TCTGAGAGT	CTCAACAA	GAATGAGACCTTTG	GGTGG	360		
Db	301	GTCCTTTG	GGGGCTGCGCTGTGTG	TCTGAGAGT	CTCAACAA	GAATGAGACCTTTG	GGTGG	360		
QY	361	CAACTG	CAGATTG	TGAGATG	TGCGCCTACT	CTGGAGACAGT	CTGGCTGA	ATCCAC	420	
Db	361	CAACTG	CAGATTG	TGAGATG	TGCGCCTACT	CTGGAGACAGT	CTGGCTGA	ATCCAC	420	
QY	421	AGTGGGGG	CTGGGCGAGTTC	ACAGCTCTA	TACCGGGG	ACGGGGCCCTTG	AGAGAG	CG	480	
Db	421	AGTGGGGG	CTGGGCGAGTTC	ACAGCTCTA	TACCGGGG	ACGGGGCCCTTG	AGAGAG	CG	480	
QY	481	CGTCTG	CGGGAGGGGAACT	GGGCAT	CACTGAG	ACA	GTGCTGA	CGGGGGCCGTGG	CACTG	540
Db	481	CGTCTG	CGGGAGGGGAACT	GGGCAT	CACTGAG	ACA	GTGCTGA	CGGGGGCCGTGG	CACTG	540
QY	541	GGGGCC	CTGTAACTGT	ATGAGGGG	CCCTTTTGTG	CTAGCA	AGT	581		
Db	541	GGGGCC	CTGTAACTGT	ATGAGGGG	CCCTTTTGTG	CTAGCA	AGT	581		

RESULT 4					
LOCUS	AY185100	1110 bp	mRNA	linear	ROD 24-JUN-2003
DEFINITION	Rattus norvegicus BCL-WEL mRNA, complete cds.				
ACCESSION	AY185100				
VERSION	AY185100.1	GI:32185284			
KEYWORDS					
SOURCE					
ORGANISM	Rattus norvegicus (Norway rat)				
	Rattus norvegicus				
	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
	1 (bases 1 to 1110)				
REFERENCE	Itch T., Itob A. and Pleasure D.				
AUTHORS	Bcl-2-related protein family gene expression during				
TITLE	oligodendroglial differentiation				
JOURNAL	J. Neurochem. 85 (6), 1500-1512 (2003)				
MEDLINE	22672518				

PUBMED 12787069  
REFERENCE 2 (bases 1 to 1110)  
AUTHORS Itch, T., Itch, A. and Pleasure, D.  
TITLE Direct Submission  
JOURNAL Submitted (21-Nov-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA

FEATURES  
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CDS

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509 ATGGGAGCCCGACCTCAACCCAGACACAGCGGCTAGTGACTTTGTAGCTAT 568  
61 AAGCTGAGCAGAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGAC 120  
569 AAGCTGAGCAGAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGAC 628  
121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180  
629 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 688  
181 TTCTCTGACCTGCGCTAGCTACAGTCAACCCAGCTCAGCCAGCAAGCTTAC 240  
689 TTCTCTGACCTGCGCTAGCTACAGTCAACCCAGCTCAGCCAGCAAGCTTAC 748  
241 CAGGTTTCCGAGCACTTTTCCAGGGGCGCTTACTGGGCGCTTGTGCAATTTT 300  
749 CAGGTTTCCGAGCACTTTTCCAGGGGCGCTTACTGGGCGCTTGTGCAATTTT 808  
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361 CAGTGCAGAGTATGATGTGCTGCTAGAGACAGTCTGCTGCTGCTGCTGCTG 420  
869 CAGTGCAGAGTATGATGTGCTGCTAGAGACAGTCTGCTGCTGCTGCTGCTG 928  
421 AATGGGGGCTGGGCGAGTTCAAGCTCTAATACGGGAGCGGGCGCTTGGAGG 480  
929 AATGGGGGCTGGGCGAGTTCAAGCTCTAATACGGGAGCGGGCGCTTGGAGG 988  
481 CATTGCGGGAGAGGAGACAGTGGGAGTGAAGAGACAGTGGGAGAGGAGAG 540  
989 CATTGCGGGAGAGGAGACAGTGGGAGTGAAGAGACAGTGGGAGAGGAGAG 1048  
541 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAGTG 581  
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ORIGIN

Query Match 97.2% Score 565; DB 10; Length 1110;  
Best Local Similarity 98.3% Pred. No. 3.9e-127;  
Matches 571; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 509 ATGGGAGCCCGACCTCAACCCAGACACAGCGGCTAGTGACTTTGTAGCTAT 568  
QY 61 AAGCTGAGCAGAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGAC 120  
DB 569 AAGCTGAGCAGAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGAC 628  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180  
DB 629 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 688  
QY 181 TTCTCTGACCTGCGCTAGCTACAGTCAACCCAGCTCAGCCAGCAAGCTTAC 240  
DB 689 TTCTCTGACCTGCGCTAGCTACAGTCAACCCAGCTCAGCCAGCAAGCTTAC 748  
QY 241 CAGGTTTCCGAGCACTTTTCCAGGGGCGCTTACTGGGCGCTTGTGCAATTTT 300  
DB 749 CAGGTTTCCGAGCACTTTTCCAGGGGCGCTTACTGGGCGCTTGTGCAATTTT 808  
QY 301 GTCTTTGGGGGCGCTTGTGCTGAGAGTCAACAAGAAATGAGCCTTGGTGGG 360  
DB 809 GTCTTTGGGGGCGCTTGTGCTGAGAGTCAACAAGAAATGAGCCTTGGTGGG 868  
QY 361 CAGTGCAGAGTATGATGTGCTGCTAGAGACAGTCTGCTGCTGCTGCTGCTG 420  
DB 869 CAGTGCAGAGTATGATGTGCTGCTAGAGACAGTCTGCTGCTGCTGCTGCTG 928  
QY 421 AATGGGGGCTGGGCGAGTTCAAGCTCTAATACGGGAGCGGGCGCTTGGAGG 480  
DB 929 AATGGGGGCTGGGCGAGTTCAAGCTCTAATACGGGAGCGGGCGCTTGGAGG 988  
QY 481 CATTGCGGGAGAGGAGACAGTGGGAGTGAAGAGACAGTGGGAGAGGAGAG 540  
DB 989 CATTGCGGGAGAGGAGACAGTGGGAGTGAAGAGACAGTGGGAGAGGAGAG 1048  
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DB 1049 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAGTG 1089

RESULT 5  
AY185098 3487 bp mRNA linear ROD 24-JUN-2003  
LOCUS

DEFINITION Rattus norvegicus BCL-W mRNA, complete cds.  
ACCESSION AY185098  
VERSION AY185098.1 GI:32185280  
KEYWORDS  
SOURCE  
ORGANISM Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurgnathi; Muridae; Murinae;  
Rattus.

REFERENCE

1 (bases 1 to 3487)  
Itch, T., Itch, A. and Pleasure, D.  
Bcl-2-related protein family gene expression during  
oligodendroglial differentiation  
J. Neurochem. 85 (6), 1500-1512 (2003)

JOURNAL

PUBMED 12787069  
REFERENCE 2 (bases 1 to 3487)  
AUTHORS Itch, T., Itch, A. and Pleasure, D.  
TITLE Direct Submission  
JOURNAL Submitted (21-Nov-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA

FEATURES

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361 CAGTGCAGAGTATGATGTGCTGCTAGAGACAGTCTGCTGCTGCTGCTGCTG 420  
530 CAGTGCAGAGTATGATGTGCTGCTAGAGACAGTCTGCTGCTGCTGCTGCTG 589  
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ORIGIN

Query Match 97.2% Score 565; DB 10; Length 3487;  
Best Local Similarity 98.3% Pred. No. 3.4e-127;  
Matches 571; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 170 ATGGGAGCCCGACCTCAACCCAGACACAGCGGCTAGTGACTTTGTAGCTAT 229  
QY 61 AAGCTGAGCAGAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGAC 120  
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QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180  
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Oy	481	CCTCTCCGGGAGGGGAACTGGGCATCACTGAGAGACA GTCTGACGGGGGCGCTGGCACTG	540
Dp	650	CGTCTCGGGAGGGGAACTGGGCATCACTGAGAGACA GTCTGACGGGGGCGCTGGCACTG	709
Oy	541	GGGGCCCTGTGA CTGTAGGGGCGCTTTTGATGCAAGTG	581
Dp	710	GGGGCCCTGTGA CTGTAGGGGCGCTTTTGATGCAAGTG	750
RESULT 6			
AY170344			
LOCUS	AY170344	3473 bp	mRNA linear ROD 22-SEP-2003
DEFINITION	Mus musculus Bcl2-like protein 2 mRNA, complete cds.		
ACCESSION	AY170344		
VERSION	AY170344.2	GI:34857712	
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	1 (bases 1 to 3473)		
TITLE	Su H.-Y.		
JOURNAL	Extraction from neonatal mouse skin after IGF-1 stimulation		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 3473)		
TITLE	Su H.-Y.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1,		
AUTHORS	Hsueh Fu Road, Nei-Fu Heiang, Pingtung, Taiwan 912, Taiwan		
TITLE	3 (bases 1 to 3473)		
JOURNAL	Su H.-Y.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (22-SEP-2003) Biotechnology, Pingtung University, No. 1,		
TITLE	Hsueh Fu Road, Nei-Fu Heiang, Pingtung, Taiwan 912, Taiwan		
JOURNAL	Sequence update by submitter		
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ORIGIN			
Query Match	96.7%; Score 561.8; DB 10; Length 3473;		
Best Local Similarity	97.9%; Pred. No. 2,1e-126;		
Matches 569; Conservative	0; Mismatches 12; Indels 0; Gaps 0;		
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Dp	182	ATGGGAGCCCCAGCCTCAACCCCAACACACAGGGCTCATGAGGCTGTAAGCTAT	241
Oy	61	AAGCTAGGCACAGAAGGTTATGTCTGTGAGAGCTGGCCCTGTGGGAAGGCCACGCCGAC	120
Dp	242	CAGCTGAGGCACAGAAGGTTATGTCTGTGAGAGCTGGCCCTGTGGGAAGGCCACGCCGAC	301
Oy	121	CCGCTGCACCAAGCCATGCGGGGCTGTGGAGACGAGTTTAGAACCCGTTTCGCGGCACC	180

Db	302	CCGCTGCACCAAGCATTGCGGGCTGTCTGAGACAGAGTTGGACAGACCCGTTTCCGCGCAC	361
Qy	181	TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCCAAGCTCAGCCAGCAACGTTTCAAC	240
Db	362	TTCTCTCAGCCTGGCCGCTCAGCTTACAGTGACCCCAAGCTCAGCCAGCAACGTTTCAAC	421
Qy	241	CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCTTAAGCTGGGGCCGCTTTGTGGCAATCTTT	300
Db	422	CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCAACTGGGGCCGCTTTGTGGCAATCTTT	481
Qy	301	GTCCTTGGGGGTGCGCTGTGTGTGCTGAGAGTGTCAAAGAAATGAGACCTTTGTGGGA	360
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Qy	361	CAAGTGACAGATTGGATGTGTGGCTTAAGCTGGAGACACGTCGTGGCTACTGATCCACAC	420
Db	542	CAAGTGACAGATTGGATGTGTGGCTTAAGCTGGAGACACGTCGTGGCTACTGATCCACAC	601
Qy	421	AGTGGGGGCTGGGGGGAGTTTCAACAGCTCTTAACGGGGACGGGGGCCCTGGAGAGGACACG	480
Db	602	AGTGGGGGCTGGGGGGAGTTTCAACAGCTCTTAACGGGGACGGGGGCCCTGGAGAGGACACG	661
Qy	481	CGTCTGGGGAGGGGAACTGGGCACTCAGTAGAGACAGTGTCTGACGGGGCCGTTGACATG	540
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Qy	541	GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTACGAAGTG	581
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LOCUS	AR020779	579 bp	DNA linear PAT 05-DEC-1998
DEFINITION	Sequence 1 from patent US 5789201.		
ACCESSION	AR020779		
VERSION	AR020779.1	GI:3975394	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 579)		
AUTHORS	Guastella, J.		
TITLE	Genes coding for bcl-y a bcl-2 homologue		
JOURNAL	Patent: US 5789201-A 1 04-AUG-1998;		
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Query Match	96.6%; Score 561.4; DB 6; Length 579;		
Best Local Similarity	98.1%; Pred. No. 3.2e-126;		
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Qy	61	AAAGCTGAGGCAAGAGGTATATGTCTGTGAGACTGGCCCTGGGGAAAGCCGACGGCGAC	120
Db	61	AAAGCTGAGGCAAGAGGTATATGTCTGTGAGACTGGCCCTGGGGAAAGCCGACGGCGAC	120
Qy	121	CCGCTGACACAAAGGCATTCGGGGCTGTGAGACAGAGTTTGAGACCCGTTTCCGCGCAC	180
Db	121	CCGCTGACACAAAGGCATTCGGGGCTGTGAGACAGAGTTTGAGACCCGTTTCCGCGCAC	180
Qy	181	TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCCAAGCTCAGCCAGCAACGTTTCAAC	240
Db	181	TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCCAAGCTCAGCCAGCAACGTTTCAAC	240
Qy	241	CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCTTAAGCTGGGGCCGCTTTGTGGCAATCTTT	300

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Db 421 AGTGGGGGCTGGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGACCG 480  
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Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAG 579

RESULT 8  
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LOCUS Sequence 8 from Patent EP0932674.  
ACCESSION AX022531  
VERSION AX022531.1 GI:10046127  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
AUTHORS A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
TITLE apoptosis-controlling genes  
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;  
AMRAD OPERATIONS PTY LTD (AU)  
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ORIGIN  
Query Match 96.4%; Score 560.2; DB 6; Length 581;  
Best Local Similarity 97.8%; Pred. No. 6.2e-126;  
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCAAGCTCAACCCAGACACAGGGGCTCTGTGGCTGACTTTGTAGGCTAT 60  
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RESULT 9  
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LOCUS Sequence 8 from Patent WO9735971.  
ACCESSION AX030819  
VERSION AX030819.1 GI:10278313  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
AUTHORS A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
TITLE apoptosis-controlling genes  
JOURNAL Patent: WO 9735971-A 8 02-OCT-1997;  
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)  
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
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ORIGIN  
Query Match 96.4%; Score 560.2; DB 6; Length 581;  
Best Local Similarity 97.8%; Pred. No. 6.2e-126;  
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCAAGCTCAACCCAGACACAGGGGCTCTGTGGCTGACTTTGTAGGCTAT 60  
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 LOCUS AX481423  
 DEFINITION Sequence 37 from Patent WO02055693.  
 ACCESSION AX481423  
 VERSION AX481423.1 GI:22316337  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Krenutzer, R., Linmer, S., Rost, S. and Hadwiger, P.  
 Patent: WO 02055693-A 37 18-JUL-2002;  
 Ribopharma AG (DE)  
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Query Match 90.6%; Score 526.6; DB 6; Length 582;  
 Best Local Similarity 94.1%; Pred. No. 9.7e-118;  
 Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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 Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 11  
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 DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.  
 ACCESSION U59747  
 VERSION U59747.1 GI:1572492  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.  
 bcl-w, a novel member of the bcl-2 family, promotes cell survival  
 Oncogene 13 (4), 665-675 (1996)  
 MEDLINE 96358615  
 PUBMED 8761287  
 TITLE Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and Cory, S.  
 Direct Submission  
 Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia  
 AUTHORS  
 REFERENCES  
 JOURNAL  
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## ORIGIN

RLRGNMASVRTLTGAVALGALVTGAFASK"

Query Match 90.6%; Score 526.6; DB 9; Length 582;

Best Local Similarity 94.1%; Pred. No. 9.7e-118; Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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QY 1 ATGGGAGACCCCGCTCAACCCGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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DB 541 GGGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581
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RESULT 12

LOCUS D87461 3542 bp mRNA linear PRI 06-OCT-2001

DEFINITION Human mRNA for KIAA0271 gene, complete cds.

ACCESSION D87461

VERSION D87461.1 GI:1944417

KEYWORDS KIAA0271.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y., Ohara,O., Tanaka,A., Koriaki,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)

JOURNAL MEDLINE 97191544

PUBMED 9039502

REFERENCE 2 (bases 1 to 3542)

AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.

TITLE Direct Submission

JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan

## FEATURES

source

(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)

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## ORIGIN

Query Match 90.1%; Score 523.4; DB 9; Length 3542;

Best Local Similarity 93.8%; Pred. No. 4.7e-117; Matches 545; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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RESULT 13

AX022529  
LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 6 from Patent EP0932674.  
ACCESSION AX022529  
VERSION AX022529.1 GI:10046125  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.  
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
apoptosis-controlling genes  
Patent: EP 0932674-A 6 04-AUG-1999;  
JOURNAL AMRAD OPERATIONS PTY LTD (AU)  
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Query Match 89.8%; Score 521.8; DB 6; Length 583;  
Best Local Similarity 93.6%; Pred. No. 1.4e-116;  
Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
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DEFINITION Sequence 6 from Patent WO9735971.  
ACCESSION AX030817  
VERSION AX030817.1 GI:10278311  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.  
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
apoptosis-controlling genes  
Patent: WO 9735971-A 6 02-OCT-1997;  
JOURNAL ADAMS JERRY MCKEE (AU); HOLMGREN SHAUN P (AU); CORY SUZANNE (AU)  
; GIBSON LEONIE W (AU); AMRAD OPERATIONS PTY LTD (AU)  
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Query Match 89.8%; Score 521.8; DB 6; Length 583;  
Best Local Similarity 93.6%; Pred. No. 1.4e-116;  
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DB 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTCAACAAGAAATGAGACCTTTGGTGGGA 360  
QY 361 CAAATGACAGATTGAGTGTGGCTTAACTTGAAGACAGTCTGGCTGACTGATCCACAGC 420  
DB 361 CAAATGACAGATTGAGTGTGGCTTAACTTGAAGACAGTCTGGCTGACTGATCCACAGC 420  
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DB 421 AGTGGGGGCTGGGGGAGATTCAAGCTTATACGGGGGACGGGGCCCTGAGAGAGGCAAG 480

Search completed: March 3, 2004, 17:43:49  
Job time : 2831 secs

QY 481 CGTCTGCGGAGAGGGAATGAGGCAATGAGAGACAGTGTGACGCGGGGCGGTGACACTG 540  
DB 481 CCGTCTGCGGAGAGGGAATGAGGCAATGAGAGACAGTGTGACGCGGGGCGGTGACACTG 540  
QY 541 GGGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAGTG 581  
DB 541 GGGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAGTG 581

## RESULT 15

AR020780 579 bp DNA linear PAT 05-DEC-1998  
LOCUS AR020780  
DEFINITION Sequence 2 from patent US 5789201.  
ACCESSION AR020780  
VERSION AR020780.1 GI:3975395  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 579)  
AUTHORS Guastella, J.  
TITLE Genes coding for bcl-2 homologues  
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;  
FEATURES Location/Qualifiers  
1..579  
source /organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 89.2%; Score 518.2; DB 6; Length 579;  
Best Local Similarity 93.4%; Pred. No. 1.1e-115;  
Matches 541; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

-QY 1 ATGGGACCCCAAGCTTCAACCCCAACACACGCGGCTGTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGGACCCCAAGCTTCAACCCCAACACACGCGGCTGTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AAGCTGAGGAGAGAGGATATCTGTGAGCTGGCCCGGAGAGGCCACACAGCTGAC 120  
DB 61 AAGCTGAGGAGAGAGGATATCTGTGAGCTGGCCCGGAGAGGCCACACAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGCAC 180  
QY 121 CCACAGCAACCAAGCCATGCGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGCAC 180  
DB 121 CCACAGCAACCAAGCCATGCGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGCAC 180  
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DB 181 TTCTGTACCTGCGCGCTCACTAAGCCCAAGGCTCAAGCCCAAGGCTTCAAC 240  
QY 241 CAGGTTTCCGAGCACTTTTCAAGGGGCGCTTACTGGGGCGCTTGTGGCATTTT 300  
DB 241 CAGGTTTCCGAGCACTTTTCAAGGGGCGCTTACTGGGGCGCTTGTGGCATTTT 300  
QY 301 GTCTTGGGGCTGCGCTGTGTGCTGAGAGTCAACAAGAAATGAGCCTTTGGTGG 360  
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QY 361 CAAGTGCAGAGATGAGTGTGCTTCAAGGAGGCGCTTACTGGGGCGCTTGTGG 420  
DB 361 CAAGTGCAGAGATGAGTGTGCTTCAAGGAGGCGCTTACTGGGGCGCTTGTGG 420  
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGAGCGGGCCCTGAGAGAGGCGCG 480  
DB 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGAGCGGGCCCTGAGAGAGGCGCG 480  
QY 481 CGTCTGCGGAGAGGGAATGAGGCAATGAGAGACAGTGTGACGCGGGGCGGTGACACTG 540  
DB 481 CGTCTGCGGAGAGGGAATGAGGCAATGAGAGACAGTGTGACGCGGGGCGGTGACACTG 540  
QY 541 GGGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAG 579  
DB 541 GGGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTGCTAGCAAG 579



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## OM nucleic - nucleic search, using sw model

Run on: March 3, 2004, 14:27:07 ; Search time 397 Seconds

(without alignments)  
6217.136 Million cell updates/sec

Title: US-09-508-745-3

Perfect score: 1 atggcgacccagcctcaac.....gccttttctgtagcaagtg 581

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	581	100.0	581	2	AAx25133 Mouse bcl
2	565	97.2	582	9	ADB5296 Primary r
3	561.4	96.6	579	2	AAV28333 Rat bcl-y
4	561.4	96.6	579	2	AAV15945 Axl15945 CDNA enco
5	560.2	96.4	581	2	AAV25133 Mouse bcl
6	560.2	96.4	581	2	AAV25133 Mouse bcl
7	526.6	90.6	582	6	ABV78153 Human bcl
8	526.6	90.6	582	6	ABV78153 Human bcl
9	526.6	90.6	582	6	ABX09722 Human bcl
10	526.6	90.6	582	6	ABX09722 Human bcl
11	523.4	90.1	581	2	AAx25133 Human bcl
12	523.4	90.1	581	2	AAx25133 Human bcl
13	521.8	89.8	583	2	AAV25134 Human bcl
14	521.8	89.8	583	2	AAV25134 Human bcl
15	518.2	89.2	579	2	AAV28334 Human bcl
16	518.2	89.2	579	2	AAV28334 Human bcl
17	376	64.7	1098	2	AAV41925 Nucleotid
18	375.6	64.6	1864	6	AAV59630 Human sec
19	375.6	64.6	1864	6	AAV59630 Human sec
20	375.6	64.6	1864	6	AAV59630 Human sec
21	375.6	64.6	1864	6	AAV59630 Human sec
22	194.2	33.4	6049	6	ABL32229 Human imm
23	147.4	25.4	150	4	AAI20236 Probe #10

24	147.4	25.4	150	4	ABA65269 Human foe
25	147.4	25.4	150	4	AAI45438 Probe #14
26	147.4	25.4	150	4	ABA47382 Human bre
27	147.4	25.4	150	4	ABA32370 Probe #10
28	147.4	25.4	150	4	AAK39424 Human bon
29	147.4	25.4	150	4	AAK39424 Human bon
30	147.4	25.4	150	4	ABG39016 Human lly
31	147.4	25.4	150	5	AAI05940 Probe #59
32	147.4	25.4	150	6	ABG13513 Human gen
33	133.4	23.0	1742	4	AAV75960 Rat wild-
34	133	22.9	636	4	AAH48169 Mutant bc
35	133	22.9	702	5	AAH43464 CDNA clon
36	133	22.9	926	2	AAQ81698 Human thy
37	133	22.9	926	2	AAV40079 Bcl-XL ge
38	133	22.9	926	3	AAZ93614 Bcl-X gen
39	133	22.9	926	4	AAI51589 Human bcl
40	133	22.9	926	4	AAQ90810 Human bcl
41	133	22.9	926	6	ABK84766 Human CDN
42	133	22.9	926	7	ABT16641 Human bcl
43	133	22.9	926	9	ADD56779 Human bcl
44	133	22.9	1236	5	AAQ00247 Bcl-XL-DT
45	133	22.9	7372	2	AAV33182 Base sequ

## ALIGNMENTS

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RESULT 1
AAx25133
ID AAx25133 standard; DNA; 581 BP.
XX
AC AAx25133;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse bcl-w gene.
XX
KM Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
XX
OS Mus sp.
XX
PN MO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
(PAHL-) HALL INST MEDICAL RES WALTER & ELITA.
XX
Cory S, Adams J, Print C, Gibson L, Koentgen F,
WPI, 1999-243890/20.
P-PSDB; AAV05531.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
protein associated with Bcl-w.
XX
PS Claim 3; Page 34; 52pp; English.
XX
The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
AAV05531), a pro-survival member of the Bcl-2 family which is widely
expressed and which is essential for spermatogenesis. The invention
relates generally to a method of treatment and to an animal model for
identification of molecules and genetic sequences useful for inducing or
reducing fertility of male animals. Methods are provided for the
treatment of infertility, or for reducing fertility, by modulating
spermatogenesis. An animal model carries a mutation is at least one
allele of the human or murine bcl-w gene or in a gene associated with bcl
-w. Such animals have disorganised seminiferous tubules and are
substantially infertile, but possess no other major abnormalities as
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CC determined by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of inducing,  
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
 CC can induce infertility

XX Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 100.0%; Score 581; DB 2; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 6,5e-146;  
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGGACCCCAAGCTTCAACCCAGACACACGCGGCTCTAGAGCTGACTTTGAGCTAT 60
DB 1 ATGGGACCCCAAGCTTCAACCCAGACACACGCGGCTCTAGAGCTGACTTTGAGCTAT 60
QY 61 AAGCTGAGGACAAAGGTTATGTCGTGAGCTGCGCCCTGGGAGAGCCCGCCGAC 120
DB 61 AAGCTGAGGACAAAGGTTATGTCGTGAGCTGCGCCCTGGGAGAGCCCGCCGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGAGACGAGTTTGAGACCCGTTCCGCGAC 180
DB 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGAGACGAGTTTGAGACCCGTTCCGCGAC 180
QY 181 TTCTGTGACCTGCGCGCTCAGCTACACGTGACCCCGAGCTCAGCCAGCAAGCTTAC 240
DB 181 TTCTGTGACCTGCGCGCTCAGCTACACGTGACCCCGAGCTCAGCCAGCAAGCTTAC 240
QY 241 CAGGTTTCCGAGCAACTTTTCCAGAGGGGCGCCCTTACTGAGGCGCTTGTGCAATTC 300
DB 241 CAGGTTTCCGAGCAACTTTTCCAGAGGGGCGCCCTTACTGAGGCGCTTGTGCAATTC 300
QY 301 GCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGGTGGGA 360
DB 301 GCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGGTGGGA 360
QY 361 CAAGTGCAGAGTTGATGATGAGCTTACCTGAGACACAGTCTGAGCTGACTGATCCACAC 420
DB 361 CAAGTGCAGAGTTGATGATGAGCTTACCTGAGACACAGTCTGAGCTGACTGATCCACAC 420
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DB 481 CGCTGCGGAGGAGGAACTGGGCACTGAGAGGACAGTCTGACGGGGCGGTCGACCTG 540
QY 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581
DB 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 2
ADB52996
ID ADB52996 standard; DNA; 582 BP.
XX
AC ADB52996;
XX
DT 04-DEC-2003 (first entry)
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.
XX
XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX toxicity marker; toxicity progression; drug screening;
XX primary rat hepatocyte toxicity modelling; gene; ds.
OS Rattus norvegicus.
XX
PN WO2003065993-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-US003482.

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XX 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
DR WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of tox mean and non-tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3538; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC comparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the tox mean and non-tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 97.2%; Score 565; DB 9; Length 582;
Best Local Similarity 98.3%; Pred. No. 1.3e-141;
Matches 571; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTTCAACCCAGACACACGCGGCTCTAGAGCTGACTTTGAGCTAT 60
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QY 61 AAGCTGAGGACAAAGGTTATGTCGTGAGCTGCGCCCTGGGAGAGCCCGCCGAC 120
DB 61 AAGCTGAGGACAAAGGTTATGTCGTGAGCTGCGCCCTGGGAGAGCCCGCCGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGAGACGAGTTTGAGACCCGTTTCCGCGAC 180
DB 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGAGACGAGTTTGAGACCCGTTTCCGCGAC 180
QY 181 TTCTGTGACCTGCGCGCTCAGCTACACGTGACCCCGAGCTCAGCCAGCAAGCTTAC 240
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DB 241 CAGGTTTCCGAGCAACTTTTCCAGAGGGGCGCCCTTACTGAGGCGCTTGTGCAATTC 300

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Db 241 CAGGTTCCGACGAACTTTCCAGAGGGGGCCCACTGGGGCCGTTGTGCAATTCCTT 300
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Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
Qy 361 CAAGTGCAGATTGGATGTGGCCCTACCTGGAGACAGCTGCGGCTGACTGTGATCCACAGC 420
Db 361 CAAGTGCAGATTGGATGTGACTCACTCTGGAGACACCGCTGGCTGACTGTGATCCACAGC 420
Qy 421 AGTGGGGCTGGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGCAAGG 480
Db 421 AGTGGGGCTGGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGCAAGG 480
Qy 481 CGTCTGCGGGAGGGGAACTGGGCATCACTGAGAGACAGTCTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGGAGGGGAACTGGGCATCACTGAGAGACAGTCTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGTGAAGTGTAGGGGGCCTTTTTGTGCTAGCAAGTG 581
Db 541 GGGGCCCTGTGAAGTGTAGGGGGCCTTTTTGTGCTAGCAAGTG 581

RESULT 3
AAV28333
ID AAV28333 standard; cDNA, 579 BP.
AC AAV28333;
AAV28333;
DT 02-OCT-1998 (first entry)
XX
XX Rat bcl-y gene.
XX
XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..579
XX FT /*tag= a
XX FT /product= "bcl-y"
XX FT /note= "No stop codon given"
XX
XX US5789201-A.
XX
XX 04-AUG-1998.
XX
XX 11-FEB-1997; 97US-00798897.
XX
XX 23-FEB-1996; 96US-0012201P.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI; 1998-446079/38.
XX
XX P-PSDB; AAW61391.
XX
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
XX recombinant protein for use in treating uncontrolled cell growth e.g.
XX cancers.
XX
XX Claim 2; Column 13/14; 27p; English.
XX
XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX family, components in the cell death pathway. The bcl-2 family have both
XX apoptotic activity and the apoptosis blocking activity. bcl-y falls in
XX the apoptosis activity category. The recombinant protein may be used to
XX prevent uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired
XX
```

```
Seq Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
Query Match 96.6%; Score 561.4; DB 2; Length 579;
Best Local Similarity 98.1%; Pred. No. 1.2e-140;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ATGGCAGACCCAGGCTCAACCCCGACACACAGGGGCTCTAGTGTGCTGACTTTGTAGGCTAT 60
Db 1 ATGGCAGACCCAGGCTCAACCCCGACACACAGGGGCTCTAGTGTGCTGACTTTGTAGGCTAT 60
Qy 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGAGTGGCCCTGGAGAGGCCCGCCGAC 120
Db 61 AAGCTGAGACGAAGGGTTATGTCTGTGAGAGTGGCCCTGGAGAGGCCCGCCGAC 120
Qy 121 CCGCTGCACCAAGCATGCGGGCTGCTGAGAGACGATTTGAGACCCGTTTCCGCCGAC 180
Db 121 CCGCTGCACCAAGCATGCGGGCTGCTGAGAGACGATTTGAGACCCGTTTCCGCCGAC 180
Qy 181 TTCTGTGACCTGGGCGGCTCAAGCTACAGCTGACAGCCCGACGCTCAGCCAGCAACGCTTAC 240
Db 181 TTCTGTGACCTGGGCGGCTCAAGCTACAGCTGACAGCCCGACGCTCAGCCAGCAACGCTTAC 240
Qy 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGGCCCTAACTGGGGCCGTCTTGTGCAATTCCTT 300
Db 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGGCCCGCAACTGGGGCCGTCTTGTGCAATTCCTT 300
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
Qy 361 CAAGTGCAGATTGGATGTGGAGCTTACCTGAGAGACAGCTGCTGACTGTGATCCACAGC 420
Db 361 CAAGTGCAGATTGGATGTGAGTGAAGCTTACCTGAGAGACAGCTGCTGACTGTGATCCACAGC 420
Qy 421 AGTGGGGCTGGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGCAAGG 480
Db 421 AGTGGGGCTGGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGCAAGG 480
Qy 481 CGTCTGCGGGAGGGGAACTGGGCATCACTGAGAGACAGTCTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGGAGGGGAACTGGGCATCACTGAGAGACAGTCTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGTGAAGTGTAGGGGGCCTTTTTGTGCTAGCAAG 579
Db 541 GGGGCCCTGTGAAGTGTAGGGGGCCTTTTTGTGCTAGCAAG 579

RESULT 4
AAI15945
ID AAI15945 standard; cDNA, 579 BP.
AC AAI15945;
AAI15945;
DT 20-MAY-1999 (first entry)
XX
XX cDNA encoding the rat bcl-y protein.
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
XX ss.
XX
XX Rattus sp.
XX
XX US5883229-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-00978523.
XX
```

```
XX 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX MPI: 1999-214150/18.
XX P-PSDB; AAW97391.
DR Novel bcl-Y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
XX Disclosure; Col 13-16; 26pp; English.
XX
XX The present sequence encodes rat bcl-Y protein (Rbcl-Y). The
XX specification also describes human bcl-Y protein (Hbcl-Y). Rbcl-Y and
XX Hbcl-Y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-Y and Hbcl-Y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended
XX period. In contrast, if they act as cell death stimulators, Rbcl-Y and
XX Hbcl-Y may be used to treat conditions associated with prolonged cell
XX life span such as cancer (especially Kaposi's sarcoma and lung cancer)
XX and auto/hyperimmune diseases. They may also be used to cause cell death
XX in, and hence control, parasites
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
Query Match 96.6%; Score 561.4; DB 2; Length 579;
Best Local Similarity 98.1%; Pred. No. 1.2e-140;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGGACCCCAAGCCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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DB 181 TTCTGCACTGCGCGCTCAGCTACACGTGACGCCAGCTCAGCCAGACAGCTTACCC 240
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DB 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGCGGCGCTTGTGGCATTCTTT 300
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DB 301 GTCCTTGGGCGTCCCTGTGTGCTGAGAGTTCACAAAGAAATGAGGCTTTGGTGGGA 360
QY 361 CAAGTCAGAGATTGATGTGCTCCTGAGACACAGTCTGGCTGACTGATCCACAGC 420
DB 361 CAAGTCAGAGATTGATGTGCTCCTGAGACACAGTCTGGCTGACTGATCCACAGC 420
QY 421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGAGGAGCGGGCGCTTGAGAGAGCG 480
DB 421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGAGGAGCGGGCGCTTGAGAGAGCG 480
```

```
QY 481 CGTCTGCGGAGAGGGGAACTGGGCACTAGTGAGAGACAGTGTGACGGGGCGCTGGCACTG 540
DB 481 CGTCTGCGGAGAGGGGAACTGGGCACTAGTGAGAGACAGTGTGACGGGGCGCTGGCACTG 540
QY 541 GGGGCGCTGTTACTGTGTAGGGGCGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCGCTGTTACTGTGTAGGGGCGCTTTTGTGCTAGCAAG 579
RESULT 5
AAT96578
ID AAT96578 standard; DNA; 581 BP.
AC AAT96578;
XX
XX 22-APR-1998 (first entry)
XX
XX Mouse bcl-w DNA.
XX
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..507
XX /tag= a
XX /product= "bcl-w"
XX /note= "q"
XX
XX WO9735971-A1.
XX
XX 02-OCT-1997.
XX
XX 27-MAR-1997; 97WO-AU000199.
XX
XX 27-MAR-1996; 96AU-00008965.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
XX MPI: 1997-489635/45.
XX
XX P-PSDB; AAW36048.
XX
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
XX inhibit cell survival, e.g. for treatment of cancer and degenerative
XX diseases.
XX
XX Claim 3; Page 50-51; 86pp; English.
XX
XX This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
XX family. This gene promotes cell survival, so its modulation is useful in
XX treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
XX stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
XX hypoxia, ischaemia, human immunodeficiency virus infection or in cell
XX transplants. Up-regulation of the gene can also be used to modify cell
XX lines cultured in vivo, e.g. to develop new lines, to facilitate
XX isolation of hybridomas and to increase survival of primary explants
XX during genetic modification. It can be used to produce recombinant bcl-w
XX for therapy, diagnosis, antibody production or screening of potential
XX modulators
XX
SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;
Query Match 96.4%; Score 560.2; DB 2; Length 581;
Best Local Similarity 97.8%; Pred. No. 2.5e-140;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGGACCCCAAGCCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
```

QY	61	AAGCTGAGAGCAAGGGTTATGTCGTGGAGCTGGCGCTGGGGAAAGCCACGCGCGAC	120
Db	61	AGGCTAGAGCAAGAGGTTATGTCGTGGAGCTGGGGAAAGCCACGCGCGAC	120
QY	121	CCGCTGACCAAGCCATGGCGGCTGCTGAGAGACGATTTTGAGACCCGTTTCGCGCAC	180
Db	121	CCGCTGACCAAGCCATGGCGGCTGCTGAGAGACGATTTTGAGACCCGTTTCGCGCAC	180
QY	181	TTCTCTGACCTGGCCGCTTAGCTACACGTGACCCCAAGGCTCAGCCACGAAAGCTTCACC	240
Db	181	TTCTCTGACCTGGCCGCTTAGCTACACGTGACCCCAAGGCTCAGCCACGAAAGCTTCACC	240
QY	241	CAGGTTTCCGACGAATCTTTCCAAAGGGGCGCCCTAACCTGGGGCGCTTTGTGCAATCTTT	300
Db	241	CAGGTTTCCGACGAATCTTTCCAAAGGGGCGCCCTAACCTGGGGCGCTTTGTGCAATCTTT	300
QY	301	GTCCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCCACAAAGAAATGGAAGCTTTGGTGGGA	360
Db	301	GTCCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCCAAAGAAATGGAAGCTTTGGTGGGA	360
QY	361	CAAGTGACAGATTTGGATGGTGGCTACCTGAGAGACAGTCTGGCTACTAGGATCCACAGC	420
Db	361	CAAGTGACAGATTTGGATGGTGGCTACCTGAGAGACAGTCTGGCTACTAGGATCCACAGC	420
QY	421	AGTGGGGGCTGGGCGAGTTCAACAGCTCTAATACGGGGACGGGGCCCTGAGAGAGGCAACG	480
Db	421	AGTGGCGGCTGGGCGAGTTCAACAGCTCTAATACGGGGACGGGGCCCTGAGAGAGGCAACG	480
QY	481	CGTCGCGGGAGGGGAACTGGGCATCAGAGAGACAGTCTGACGGGGGCGGTGGCACTG	540
Db	481	CGTCGCGGGAGGGGAACTGGGCATCAGAGAGACAGTCTGACGGGGGCGGTGGCACTG	540
QY	541	GGGGGCTCTGTTAAGTGTAGGGGCTTTTTCCTAGCAAGTG	581
Db	541	GGGGGCTCTGTTAAGTGTAGGGGCTTTTTCCTAGCAAGTG	581

XX	RESULT 6
XX	AA25135
XX	ID AA25135 standard; DNA; 581 BP.
XX	AA25135;
XX	05-JUL-1999 (first entry)
XX	Mouse bcl-w gene derivative.
XX	Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
XX	animal model; ss.
XX	Mus sp.
XX	Key
XX	Location/Qualifiers
XX	1..507
XX	CDS
XX	/*tag= a
XX	MO9913710-A1.
XX	25-MAR-1999.
XX	16-SEP-1998; 98MO-AU000764.
XX	16-SEP-1997; 97AU-00009228.
XX	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX	Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX	WPI; 1999-243890/20.
XX	P-PSDB; AA105533.
XX	An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX	protein associated with Bcl-w.

XX Disclosure; Page 38; 52pp; English.

XX

CC The present sequence is described as a derivative of the mouse bcl-w gene  
CC (see AAX251133) and encodes Bcl-w protein (see AA0Y05533), a pro-survival  
CC member of the Bcl-2 family which is widely expressed and which is  
CC essential for spermatogenesis. The invention relates generally to a  
CC method of treatment and to an animal model for the identification of  
CC molecules and genetic sequences useful for inducing or reducing fertility  
CC of male animals. Methods are provided for the treatment of infertility,  
CC or for reducing fertility, by modulating spermatogenesis. An animal model  
CC carries a mutation in at least one allele of the human or murine bcl-w  
CC gene or in a gene associated with bcl-w. Such animals have disorganised  
CC seminiferous tubules and are substantially infertile, but possess no other  
CC major abnormalities as determined by histological examination. They can  
CC be used to screen for therapeutic molecules including genetic sequences  
CC capable of inducing, enhancing or otherwise facilitating spermatogenesis  
xx in animals, or which can induce infertility

SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Query Match 96.4%; Score 560.2; DB 2; Length 581;  
Best Local Similarity 97.8%; Pred. No. 2.5e+140;  
Matches 568; Conservative 13; Indels 0; Gaps 0;

QY	1	ATGGGGAACCCAGGCTTCAACCCBACAACA	CGGGCTCTAGTGGCTGACCTTTGAGGCTAT	60
Db	1	ATGCCAACCCAGGCTCAACCCBACAACA	CGCGCTCTTAGTGGCTGACCTTTGAGGCTAT	60
QY	61	AAGCTGAGGCAAGAGGTTATGTCTGTGAG	AGCTGGCCCTGGGGAAAGGCCACGCCGAC	120
Db	61	AGGCTGAGGCAAGAGGTTATGTCTGTGAG	AGCTGGGACCTGGGGAAAGGCCACGCCGAC	120
QY	121	CCGCTGCACCAAGCCATGCGGGCTGCTTGA	AGACGAGTTTGAAACCCGCTTTCCGCCGAC	180
Db	121	CCGCTGCACCAAGCCATGCGGGCTGCTTGA	AGACGAGTTTGAAACCCGCTTTCCGCCGAC	180
QY	181	TTTCTGTACATGGGCGCTCAGCTACAGG	AGCCAGCCAGCCAGCAAGCTTCACC	240
Db	181	TTTCTGTACCTGGCGCTCAGCTACAGT	AGCCAGCCAGCCAGCAAGCTTCACC	240
QY	241	CAGGTTTCCGACGAATCTTTCGAAGGG	GGGCCCTTA	300
Db	241	CAGGTTTCCGACGAATCTTTCGAAGGG	GGGCCCTTA	300
QY	301	GTCCTTGGGGCTGCCCCTGTGTGCTGAG	AGTGTCAACAAAGAAATGAGCTTTTGGTGG	360
Db	301	GTCCTTGGGGCTGCCCCTGTGTGCTGAG	AGTGTCAACAAAGAAATGAGCTTTTGGTGG	360
QY	361	CAAGTGCAGGATTTGGATGTGTGGCTTA	CCTGAGAGACAGTCTTGGCTGATTCACAC	420
Db	361	CAAGTGCAGGATTTGGATGTGTGGCTTA	CCTGAGAGACAGTCTTGGCTGATTCACAC	420
QY	421	AGTGGGGAGCTGGGCGGAGTTCA	CAGCTCTATACGGGGACCGGGGCCCTGG	480
Db	421	AGTGGGGAGCTGGGCGGAGTTCA	CAGCTCTATACGGGGACCGGGGCCCTGG	480
QY	481	CGTTCGCGGAGGGGCACTGGGCAT	CAGTGAAGACAGTCTGACGGGGCCGTGG	540
Db	481	CGTTCGCGGAGGGGCACTGGGCAT	CAGTGAAGACAGTCTGACGGGGCCGTGG	540
QY	541	GGGGCCCTGTGTA	CTGTAGGGGCTTTTGTCTACCAAGTG	581
Db	541	GGGGCCCTGTGTA	CTGTAGGGGCTTTTGTCTACCAAGTG	581

RESULT 7	
ABV78153	
ID	ABV78153 standard; DNA; 562 BP.
XX	
AC	
XX	
ABV78153;	
XX	
DT	15-NOV-2002 (first entry)

```
XX Human bcl-w DNA SEQ ID NO 37.
DE RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cyrostatic;
KM virucide; protozoacide; gene; ds.
XX Homo sapiens.
OS WO200255693-A2.
XX 18-JUL-2002.
XX 09-JAN-2002; 2002WO-EP000152.
XX 09-JAN-2001; 2001DE-01000586.
XX 26-OCT-2001; 2001DE-01055280.
XX 29-NOV-2001; 2001DE-01058411.
XX 07-DEC-2001; 2001DE-01060151.
XX (RIBO-) RIBOPHARMA AG.
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-590671/63.
XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX Claim 10; Page 134; 203pp; German.
XX The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (i) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
SQ
Query Match 90.6%; Score 526.6; DB 6; Length 582;
Best Local Similarity 94.1%; Pred. No. 2.6e-131;
Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 ATGGGCAAGCCCAAGCTCAACCCAGACACAGGGGCTCTAGTGCGTCACTTTGTAGGCTAT 60
DB 1 ATGGGCAAGCCCAAGCTCGGCGCCAGACACAGGGGCTCTAGTGCGTCACTTTGTAGGCTAT 60
PS 61 AAGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCGCCCTGGGGAGAGGCCACCGCCGAC 120
QY 61 AAGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCGCCCTGGGGAGAGGCCACCGCCGAC 120
DB 61 AAGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCGCCCTGGGGAGAGGCCACCGAGCTGAC 120
QY 121 CCGCTGACCAAGCAAGCTGCGGGGTGTGAGAGCAAGTTTGAAGCCCGTTCCGCGCAC 180
DB 121 CCGCTGACCAAGCAAGCTGCGGGGTGTGAGAGCAAGTTTGAAGCCCGTTCCGCGCAC 180
QY 121 CCGCTGACCAAGCAAGCTGCGGGGTGTGAGAGCAAGTTTGAAGCCCGTTCCGCGCAC 180
DB 121 CCGCTGACCAAGCAAGCTGCGGGGTGTGAGAGCAAGTTTGAAGCCCGTTCCGCGCAC 180
QY 181 TTCTGTGACCTGGCGCTGAGCTACAGTGACCCAGGCTCAAGCCAGCAAGCTTAC 240
DB 181 TTCTGTGACCTGGCGCTGAGCTACAGTGACCCAGGCTCAAGCCAGCAAGCTTAC 240
QY 181 TTCTGTGACCTGGCGCTGAGCTACAGTGACCCAGGCTCAAGCCAGCAAGCTTAC 240
DB 181 TTCTGTGACCTGGCGCTGAGCTACAGTGACCCAGGCTCAAGCCAGCAAGCTTAC 240
QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCCCTTAATCTGGGGCGCTTTGTGGCATTTT 300
DB 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCCCTTAATCTGGGGCGCTTTGTGGCATTTT 300
QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCCCTTAATCTGGGGCGCTTTGTGGCATTTT 300
DB 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCCCTTAATCTGGGGCGCTTTGTGGCATTTT 300
QY 301 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGTCAACAAAGAAATGAGGCTTTGTGGGA 360
DB 301 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGTCAACAAAGAAATGAGGCTTTGTGGGA 360
```

```
QY 361 CAAGTCAGAGATTGGATGTGGCTTACCTGAGACACAGCTGTGGCTGACTGATCCACAGC 420
DB 361 CAAGTCAGAGATTGGATGTGGCTTACCTGAGACAGCGGCTGGCTGACTGATCCACAGC 420
QY 421 AGTGGGCGCTGGCGGAGCTTATACAGCTTATACGGGAGCGGGCCCTGGAGAGGACAGG 480
DB 421 AGTGGGCGCTGGCGGAGCTTATACAGCTTATACGGGAGCGGGCCCTGGAGAGGCGGCG 480
QY 481 CGTCTGCGGAGGAGGAATGAGGAGTCAAGTCAAGTCAAGGAGGCGGCTGGCACTG 540
DB 481 CGTCTGCGGAGGAGGAATGAGGAGTCAAGTCAAGTCAAGGAGGCGGCGTGGCACTG 540
QY 541 GGGGCCCTGTACTGTAGGGGCTTTTCTGTAAGCAAGTG 581
DB 541 GGGGCCCTGTACTGTAGGGGCTTTTCTGTAAGCAAGTG 581
RESULT 8
AB235729
ID AB235729 standard; DNA; 582 BP.
XX
XX AB235729;
AC AB235729;
XX
XX 07-FEB-2003 (first entry)
DT
XX
XX Human bcl-w polynucleotide SEQ ID NO 37.
DE
XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cyrostatic; virucide;
XX protozoacide; gene expression; antisense; tumor; infection; plasmodium;
XX virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
XX Hepatitis C virus; human papilloma virus; gene; ds.
XX
XX Homo sapiens.
OS
XX DE10100588-A1.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2001; 2001DE-01000588.
XX
XX 09-JAN-2001; 2001DE-01000588.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-683450/74.
XX
XX Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
XX
XX Claim 13; Page 30-31; 100pp; German.
XX The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNA1 and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNA1 and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by plasmodium or viruses/viroids (pathogenic
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX
XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
SQ
Query Match 90.6%; Score 526.6; DB 6; Length 582;
```



XX	ABL91694;
AC	
XX	
DT	28-MAY-2002 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 37.
XX	
XX	Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW	Plasmodium; virus; vitroid; cytokine; prion; antisense oligonucleotide;
XX	cytostatic; virucide; protozoacide; antibacterial; ds.
XX	
OS	Homo sapiens.
XX	
PN	DE10100586-Cl.
XX	
PD	11-APR-2002.
XX	
PF	09-JAN-2001; 2001DE-01000586.
XX	
PR	09-JAN-2001; 2001DE-01000586.
XX	
PA	(RIBO-) RIBOPHARMA AG.
XX	
PI	Kreutzter R, Limmer S, Rost S, Hadwiger P;
XX	
DR	WPI; 2002-270454/32.
XX	
PT	Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT	introducing double-stranded complementary oligoRNA having unpaired
PT	terminal bases.
XX	
PS	Claim 13; Page 32; 104pp; German.

CC The invention relates to a method for introducing expression of a target  
CC gene (AB291658-AB291797) in a cell by introducing at least one  
CC oligoribonucleotide that has a double-stranded structure consisting of at  
CC most 49 sequential nucleotide pairs, with at least part of one strand  
CC complementary with the target gene and has at least one and a single-  
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for  
CC antisense inhibition of gene expression useful e.g. for treating tumours  
CC but the oligoribonucleotides may also be directed against genes present  
CC in pathogens (e.g. Plasmodium or viruses/Viroids), pathogenic on humans,  
CC animals or plants) or against cytokine, id, developmental or prion genes  
CC The method provides more effective inhibition of gene expression than use  
CC of known oligonucleotides, probably because the unpaired overhang  
CC increases stability and thus intracellular concentration  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match	90.6%	Score 526.6	DB 6	Length 582
Best Local Similarity	94.1%	Pred. NO. 2.6e-131		
Matches 547; Conservative	0	Mismatches 34	Indels 0	Gaps 0

QY	1	ATGGCGACCCCGAGCTTCAACCCCGAGACACCGGGGCTCTAGTGGCTGACTTTGTATAGGCAT	60
QY	60	ATGGCGACCCCGAGCTTCAACCCCGAGACACCGGGGCTCTAGTGGCTGACTTTGTATAGGCAT	120
Db	1	ATGGCGACCCCGAGCTTCAACCCCGAGACACCGGGGCTCTAGTGGCTGACTTTGTATAGGCAT	60
QY	61	AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCGCTTGGGGAAAGGCCACAGCGCGAC	120
Db	61	AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCGCTTGGGGAAAGGCCACAGCGCGAC	120
QY	121	CCGCTGACCAAGCATGCGGGGCTGTGGAGACGATTTGAACCCGTTTCCGCGGAC	180
QY	121	CCGCTGACCAAGCATGCGGGGCTGTGGAGAGATTGAGAACCCCGTTCCGCGGAC	180
Db	121	CCGCTGACCAAGCATGCGGGGCTGTGGAGAGATTGAGAACCCCGTTCCGCGGAC	180
QY	181	TTCTCTGACCTGGCGGCTCAGCTAACGTCGACCCAGGCTCAGCCAGCAACGCTTCA	240
Db	181	TTCTCTGATCTGGGGGCTCAGCTGACATGTGACCCCAAGGCTCAGCCAGCAACGCTTCA	240
QY	241	CAGGTTTCCGACGAACTTTCCAAAGGGGGGCCCTAACTGGGGGCGCTTGTGGCAATCTTT	300
Db	241	CAGGTTTCCGACGAACTTTTTCAAAGGGGGGCCCAACTGGGGGCGGCTTGTAGCTTCTTT	300
QY	301	GTCCTTGGGGCTGGCGCTGTGTCGAGAGTGTCAACAAAGAAATGAGACTTTGGTGGGA	360

Accession	Gene	Position	Sequence	Length
D8	GTCTTTGGGGCTGCATCTGTGCTGAGATGCAACAGAGAGATGGAACTCTGTTGGGA	3601		3602
QY	CAAGTCGAGGATTTGATTTGGTGGCTTACCGGAGACAGCTCAGGCTGACTGGATCCAGC	361		4202
D8	CAAGTCGAGGAGTGGATTTGTGGCTTACTCTGGAGACCGGGCTGGCTGACTGGATCCAGC	361		4202
QY	AGTGGGGGCTGGGGGAGTTTCAACAGCTCTATTACGGGGACGGGGCCCTGGAGAGGCAACGG	421		4802
D8	AGTGGGGGCTGGGGGAGTTTCAACAGCTCTATTACGGGGACGGGGCCCTGGAGAGGCGCGG	421		4802
QY	CGTCTGGGGAGGGGAACTGGCATCTAGTGAAGGACAGTGTCTGACGGGGGCGTGGCACTG	481		5402
D8	CGTCTGGGGAGGGGAACTGGCATCTAGTGAAGGACAGTGTCTGACGGGGGCGTGGCACTG	481		5402
QY	GGGGCCCTGTAACTGTAGGGCCCTTTTGTGTTACCAAGT	541		581
D8	GGGGCCCTGTAACTGTAGGGCCCTTTTGTGTTACCAAGT	541		581

## RESULT 11

ID AAX25132 standard; DNA; 581 BP

AC AAX25132;

DT 05-JUL-1999 (first entry)

Human *bcl-w* gene.

KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;

XX

XX

XX

XX

XX

XX

XX

XX

DR P-PSDB; AAY05

PT An animal model

2 XX

2

CC AAY05530), a

CC relates general

CC reducing fert

CC spermatogenesis

-w. Such anim

CC determined by

CC enhancing or

XX

The present sequence is the human bcl-w gene family Bcl-w protein (see AY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.



Query Match 90.1%; Score 523.4; DB 2; Length 581;  
 Best Local Similarity 93.8%; Pred. No. 1.8e-130;  
 Matches 545; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGCTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
 DB 1 ATGGCGACCCCGCTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

QY 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120  
 DB 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCGACAGCTTAC 120

QY 121 CCGCTGACCAAGCATGCGGGCTGTGAGACAGATTGACCCGTTCCGGCGAC 180  
 DB 121 CCGCTGACCAAGCATGCGGGCTGTGAGACAGATTGACCCGTTCCGGCGAC 180

QY 181 TTCTGTGACCTGGCGCTCAGCTACACGTGACCCGAGGCTGACCCAGCAACGCTTACC 240  
 DB 181 TTCTGTGACCTGGCGCTCAGCTGATGTGACCCGAGCTGACCCAGCAACGCTTACC 240

QY 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTCT 300  
 DB 241 CAGGTTCCGATGAATTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTCT 300

QY 301 GTCCTTGGGGCTGCGCTGTGTGAGAGTGAAGTCAAGAAATGAGAGCTTTGGTGGGA 360  
 DB 301 GTCCTTGGGGCTGCGCTGTGTGAGAGTGAAGTCAAGAAATGAGAGCTTTGGTGGGA 360

QY 361 CAACTGACAGATTGGATGTGGCTTACCTGAGACACGCTGTGCTGATGATCCACAGC 420  
 DB 361 CAACTGACAGATTGGATGTGGCTTACCTGAGACACGCGCTGTGCTGATGATCCACAGC 420

QY 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGGGGGCGCTTGGAGAGGCAAG 480  
 DB 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGGGGGCGCTTGGAGAGGCAAG 480

QY 481 CGTGTGGGGGAGGGGAACTGGGCACTGAGAGACAGTGTGACGGGGGCGCTGGCACTG 540  
 DB 481 CGTGTGGGGGAGGGGAACTGGGCACTGAGAGACAGTGTGACGGGGGCGCTGGCACTG 540

QY 541 GGGGCGCTGTGATGTAGGGGCTTTTGTCTAGCAAGTG 581  
 DB 541 GGGGCGCTGTGATGTAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 12  
 ABL16642  
 ID ABL16642 standard; DNA; 3542 BP.

XX AC ABL16642;  
 XX DT 03-APR-2003 (first entry)  
 XX DE Human bcl-2 gene SEQ ID No 4.  
 XX KW Anti-tumour; DNzyme; bcl-2 gene; tumour; malignant; chemotherapy;  
 XX KM radiation therapy; catalytic domain; enzyme; human; ds.  
 XX OS Homo sapiens.  
 XX PN WO200299090-A1.  
 XX PD 12-DEC-2002.  
 XX PF 07-JUN-2002; 2002WO-AU000739.  
 XX PR 07-JUN-2001; 2001AU-00005527.  
 XX PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.  
 XX PI Sun L, Wang L, Turner RJ, Saravolac EG, Daas CR;  
 XX WPI: 2003-140617/13.

XX Novel DNzyme useful for treating tumors, and for enhancing the  
 PT sensitivity of malignant or virus infected cells to therapy, comprises a  
 PT catalytic domain and binding domain contiguous to the catalytic domain.  
 XX Disclosure; Page 44-45; 67P; English.

CC The invention relates to a DNzyme which specifically cleaves mRNA  
 CC transcribed from a member of the bcl-2 gene family. The DNzymes comprise  
 CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
 CC the catalytic domain, and therefore hybridise with, the two regions  
 CC immediately flanking the purine residue of the cleavage site within the  
 CC bcl-2 gene family mRNA, at which DNzyme-catalysed cleavage is desired. A  
 CC pharmaceutical composition comprising a DNzyme of the invention is  
 CC useful for treating tumors in a subject, and for enhancing the  
 CC sensitivity of malignant or virus infected cells infected cells to  
 CC therapy. The DNzymes are useful in diagnostics, therapeutics,  
 CC prophylaxis, research agents and in kits. The DNzymes are also useful  
 CC for increasing the susceptibility of tumour cells to anti-tumour  
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
 CC sequence represents a human bcl-2 gene of the invention

XX  
 XX Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 90.1%; Score 523.4; DB 7; Length 3542;  
 Best Local Similarity 93.8%; Pred. No. 3.2e-130;  
 Matches 545; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGCTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
 DB 177 ATGGCGACCCCGCTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 236

QY 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120  
 DB 237 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCGACAGCTGAC 296

QY 121 CCGCTGACCAAGCATGCGGGCTGTGAGAGACAGATTGAGACCCGTTCCGGCGAC 180  
 DB 297 CCGCTGACCAAGCATGCGGGCTGTGAGAGACAGATTGAGACCCGTTCCGGCGAC 356

QY 181 TTCTGTGACCTGGCGCTCAGCTACACGTGACCCGAGGCTGACCCAGCAACGCTTACC 240  
 DB 357 TTCTGTGACCTGGCGCTCAGCTGATGTGACCCGAGGCTGACCCAGCAACGCTTACC 416

QY 301 GTCCTTGGGGCTGCGCTGTGTGAGAGTGAAGTCAAGAAATGAGAGCTTTGGTGGGA 360  
 DB 477 GTCCTTGGGGCTGCGCTGTGTGAGAGTGAAGTCAAGAAATGAGAGCTTTGGTGGGA 536

QY 361 CAACTGACAGATTGGATGTGGCTTACCTGAGACACGCTGTGCTGACTGGATCCACAGC 420  
 DB 537 CAACTGACAGATTGGATGTGGCTTACCTGAGACACGCGCTGTGCTGACTGGATCCACAGC 596

QY 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGGGGAAGGGGCGCTTGGAGAGGCAAG 480  
 DB 597 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGGGGAAGGGGCGCTTGGAGAGGCAAG 656

QY 481 CGTGTGGGGGAGGGGAACTGGGCACTGAGAGGACATGTGCTGAGAGGGGCGCTGGCACTG 540  
 DB 657 CGTGTGGGGGAGGGGAACTGGGCACTGAGAGGACATGTGCTGAGAGGGGCGCTGGCACTG 716

QY 541 GGGGCGCTGTGATGTAGGGGCTTTTGTCTAGCAAGTG 581  
 DB 717 GGGGCGCTGTGATGTAGGGGCTTTTGTCTAGCAAGTG 757

RESULT 13  
 AAT96577  
 ID AAT96577 standard; DNA; 583 BP.

```

AC AAT96577;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w DNA.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..582
FT /tag= a
FT /product= "bcl-w"
XX
XX WO9735971-A1.
XX
XX 02-OCT-1997.
XX
XX 27-MAR-1997; 97WO-AU000199.
XX
XX 27-MAR-1996; 96AU-00008965.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
XX WPI; 1997-489635/45.
XX
XX P-PSDB; AAW36047.
XX
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
XX inhibit cell survival, e.g. for treatment of cancer and degenerative
XX diseases.
XX
XX Claim 3; Page 48; 86pp; English.
XX
XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
XX family, extracted from an adult brain library. This gene promotes cell
XX survival, so its modulation is useful in treatment of cancer or auto-
XX immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
XX myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
XX immunodeficiency virus infection or in cell transplants. Up-regulation of
XX the gene can also be used to modify cell lines cultured in vivo, e.g. to
XX develop new lines, to facilitate isolation of hybridomas and to increase
XX survival of primary explants during genetic modification. It can be used
XX to produce recombinant Bcl-w for therapy, diagnosis, antibody production
XX or screening of potential modulators.
XX
XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
XX
XX Query Match 89.8%; Score 521.8; DB 2; Length 583;
XX Best Local Similarity 93.6%; Pred. No. 5e-130;
XX Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
XX
XX 1 AATGCGACCCCGCCCTCAACCCGAGACAGCGGCTCTGAGCTTGTAGGCTAT 60
XX |||||
XX 1 ATGGCCACCCCGCCCTCGGCCGACACAGCGGCTCTGTGACACTTTGTAGGTTAT 60
XX |||||
XX 61 AAGCTAGGACAGAAAGGTTATGCTGTGAGCTGAGCTTGGGAGAGCCGACCGAC 120
XX |||||
XX 61 AAGCTAGGACAGAAAGGTTATGCTGTGAGCTGAGCTTGGGAGAGCCGACAGCTGAC 120
XX |||||
XX 121 CCGCTGACCAACAGCCATGCGGGCTGTGAGACGAGTTTGAACCCGTTTCCGCCGACC 180
XX |||||
XX 121 CCGCTGACCAACAGCCATGCGGGCTGTGAGACGAGTTTGAACCCGTTTCCGCCGACC 180
XX |||||
XX 181 TTCTCTGACCTGCGCCCTGAGCTACACGTGACCCCGAGGCTCCGACGAAAGCTTCAAC 240
XX |||||
XX 181 TTCTCTGACCTGCGCCCTGAGCTACACGTGACCCCGAGGCTCCGACGAAAGCTTCAAC 240
XX |||||
XX 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTACCTGGGGCGCTTGTGGCAATCTTT 300
XX |||||

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Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCCCACTGGGCGCCCTTGTAGCCTTCTT 300
QY 301 GTCCTTGGGCGCTGCGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGA 360
XX |||||
Db 301 CTCCTTTGGGCGCTGACTGTGTGTGAGAGTGTCAACAAGAAATGAGAACACTGGTGGA 360
XX |||||
QY 361 CAAGTGCAGAGTTGGATGTTGGCTTACCTGAGACACGCTTGGCTACTGATCCACAGC 420
XX |||||
Db 361 CAAGTGCAGAGTTGGATGTTGGCTTACCTGAGACACGCGCTGTGTGATCCACAGC 420
XX |||||
QY 421 AGTGGGCGCTGGGCGGAGTTTCAAGCTTATACGGGGAAGGGGCGCTGGAGAGCAGG 480
XX |||||
Db 421 AGTGGGCGCTGGGCGGAGTTTCAAGCTTATACGGGGAAGGGGCGCTGGAGAGCAGG 480
XX |||||
QY 481 CGTCTGCGGAGGGGAACTGGGCACTCACTGAGAGACAGTGTGACCGGGCGGTGCACTG 540
XX |||||
Db 481 CGTCTGCGGAGGGGAACTGGGCACTCACTGAGAGACAGTGTGACCGGGCGGTGCACTG 540
XX |||||
QY 541 GGGGCGCTGTACTGTAGGGGCGCTTTTTCCTAGCAAGTG 581
XX |||||
Db 541 GGGGCGCTGTACTGTAGGGGCGCTTTTTCCTAGCAAGTG 581
XX |||||

RESULT 14
AAK25134
ID AAK25134 standard; DNA; 583 BP.
XX
AC AAK25134;
XX
DT 05-JUL-1999 (first entry)
XX
XX Human bcl-w gene derivative.
XX
XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
XX animal model; ss.
XX
XX Homo sapiens.
XX
XX WO9913710-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-AU000764.
XX
XX 16-SEP-1997; 97AU-00009228.
XX
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
XX WPI; 1999-243890/20.
XX
XX P-PSDB; AAY05532.
XX
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
XX
XX Disclosure; Page 36; 52pp; English.
XX
XX The present sequence is described as a derivative of the human bcl-w gene
XX (see AAK25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
XX member of the Bcl-2 family which is widely expressed and which is
XX essential for spermatogenesis. The invention relates generally to a
XX method of treatment and to an animal model for the identification of
XX molecules and genetic sequences useful for inducing or reducing fertility
XX of male animals. Methods are provided for the treatment of infertility,
XX or for reducing fertility, by modulating spermatogenesis. An animal model
XX carries a mutation in at least one allele of the human or murine bcl-w
XX gene or in a gene associated with bcl-w. Such animals have disorganised
XX seminiferous tubules and are substantially infertile, but possess no other
XX major abnormalities as determined by histological examination. They can
XX be used to screen for therapeutic molecules including genetic sequences
XX capable of inducing, enhancing or otherwise facilitating spermatogenesis
XX in animals, or which can induce infertility

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Thu Mar 4 08:13:37 2004

us-09-508-745-3.rng

Page 12

Job time : 405 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: March 3, 2004, 16:16:09 ; Search time 83 Seconds  
(without alignments)  
3884.656 Million cell updates/sec

Title: US-09-508-745-3

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561.4	96.6	579	1	US-08-798-897-1 Sequence 1, Appli
2	561.4	96.6	579	2	US-08-978-523-1 Sequence 1, Appli
3	518.2	89.2	579	1	US-08-798-897-2 Sequence 2, Appli
4	518.2	89.2	579	2	US-08-978-523-2 Sequence 2, Appli
5	376	64.7	1098	4	US-09-010-147B-23 Sequence 130, App
6	375.6	64.6	1864	4	US-09-149-476-130 Sequence 130, App
7	133	22.9	926	1	US-08-081-448-5 Sequence 6, Appli
8	133	22.9	926	2	US-08-470-670A-6 Sequence 6, Appli
9	133	22.9	926	3	US-08-481-739-1 Sequence 1, Appli
10	133	22.9	926	3	US-09-167-921-1 Sequence 1, Appli
11	133	22.9	926	3	US-09-277-020-39 Sequence 39, Appli
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14	133	22.9	926	4	US-09-271-014A-5 Sequence 5, Appli
15	133	22.9	926	4	US-09-023-655-1430 Sequence 1430, Ap
16	133	22.9	926	5	PCT-US94-07089-6 Sequence 6, Appli
17	121.8	21.0	717	2	US-08-465-485A-20 Sequence 20, Appli
18	121.8	21.0	717	3	US-09-080-285-20 Sequence 20, Appli
19	121.8	21.0	4825	6	5459251-1 Patent No. 5459251
20	121.8	21.0	5086	2	US-08-465-485A-19 Sequence 19, Appli
21	121.8	21.0	5086	2	US-08-365-486A-14 Sequence 14, Appli
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24	121.8	21.0	5086	4	US-09-724-426-19 Sequence 19, Appli
25	121.8	21.0	5086	4	US-09-233-527-7 Sequence 7, Appli
26	121.8	21.0	5086	5	PCT-US93-05651-4 Sequence 4, Appli
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36	120.2	20.7	1303	2	US-09-271-014A-1 Sequence 1, Appli
37	120.2	20.7	1846	2	US-08-365-486A-16 Sequence 16, Appli
38	120.2	20.7	1846	3	US-08-880-342-16 Sequence 16, Appli
39	117.4	20.2	615	3	US-08-465-485A-22 Sequence 22, Appli
40	117.4	20.2	615	3	US-09-080-285-22 Sequence 22, Appli
41	117.4	20.2	911	5	PCT-US93-06251-3 Sequence 5, Appli
42	117.4	20.2	911	5	PCT-US93-06251-3 Sequence 3, Appli
43	114.2	19.7	831	6	5459251-3 Patent No. 5459251
44	114.2	19.7	831	6	5506344-4 Patent No. 5506344
45	114	19.6	1384	4	US-08-899-367-1 Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-798-897-1  
Sequence 1, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bismond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483, 0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
US-08-798-897-1  
Query Match 96.6%; Score 561.4; DB 1; Length 579;  
Best Local Similarity 98.1%; Pred. No. 5.1e-145;  
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
OY 1 ATGGCGAGCCCGGCTTAACCCGAGACACACGCGGCTTAGTGGCTGACTTTGTGGCTAT 60  
DB 1 ATGGCGAGCCCGGCTTAACCCGAGACACACGCGGCTTAGTGGCTGACTTTGTGGCTAT 60  
OY 61 AAGCTGAGCGAGGAGGTTATGTCTGTGAGAGCTGCGCTCGGAGGAGGCCGCGCGAC 120

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Db 61 AAGCTGACAGCAAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCAAGCAGCCGAC 120
Qy 121 CCGCTGCACCAAGCCATGCGGCGCTCTGTGAGACGAGTTTGAGACCCGTTTCCGGCGAC 180
Db 121 CCGCTGCACCAAGCCATGCGGCGCTCTGTGAGACGAGTTTGAGACCCGTTTCCGGCGAC 180
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Db 541 GGGGCGCTGTGTAACCTGTAGGGGCGCTTTTGTGTAACAAG 579
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RESULT 2
US-08-978-523-1
Sequence 1, Application US/0878523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gaestella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Eamond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-1
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Query Match 96.6%; Score 561.4; DB 2; Length 579;
Best Local Similarity 98.1%; Pred. No. 5,1e-145;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Qy 1 ATGGGACCCAGGCTCAACCCAGACACAGCGGCTTAGTGCTGACTTTGTAAGCTAT 60
Db 1 ATGGGACCCAGGCTCAACCCAGACACAGCGGCTTAGTGCTGACTTTGTAAGCTAT 60
Qy 61 AAGCTGACGAGAGGTTATGTCTGTGAGACTGCGCTTGGGGAAGGCCCAAGCGCGAC 120
Db 61 AAGCTGACGAGAGGTTATGTCTGTGAGACTGCGCTTGGGGAAGGCCCAAGCGCGAC 120
Qy 121 CCGCTGCACCAAGCCATGCGGCGCTCTGTGAGACGAGTTTGAGACCCGTTTCCGGCGAC 180
Db 121 CCGCTGCACCAAGCCATGCGGCGCTCTGTGAGACGAGTTTGAGACCCGTTTCCGGCGAC 180
Qy 181 TTCTGTGACCTGGCGCTCAGCTACACGTCGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Db 181 TTCTGTGACCTGGCGCTCAGCTACACGTCGACCCAGGCTCAGCCAGCAACGCTTCACC 240
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Db 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCCCTTAACTGAGGCGCTTGTGGCAATCTTT 300
Qy 301 GTCTTTGGGCGCTCCCTGTGTGCTGAGAGTTCACAAAGAAATGAGCCTTTGGTGGGA 360
Db 301 GTCTTTGGGCGCTCCCTGTGTGCTGAGAGTTCACAAAGAAATGAGCCTTTGGTGGGA 360
Qy 361 CAAGTGCAGAGATGATGATGCTGAGAGACGCTGAGCTGATCCACAGC 420
Db 361 CAAGTGCAGAGATGATGATGCTGAGAGACGCTGAGCTGATCCACAGC 420
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Db 421 AGTGGGGGCTGGGCGGAGTTTCAACGCTCTATACGGGGAAGGCGCCCTGGAGGAGCAGCG 480
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Db 481 CGTCTGCGGAGAGGGAACCTGGGCACTGATGAGAGACAGTGTCTGACGCGGGCGCTGGCACTG 540
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Db 541 GGGGCGCTGTGTAACCTGTAGGGGCGCTTTTGTGTAACAAG 579
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RESULT 3
US-08-798-897-2
Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gaestella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1      SOFTWARE: PatentIn Release #1.0, Version #1.0.3
2      CURRENT APPLICATION DATA:
3      APPLICATION NUMBER: US/08/798,897
4      FILING DATE: February 11, 1997
5      CLASSIFICATION: 435
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Emmond, Robert W.
8      REGISTRATION NUMBER: 32,893
9      REFERENCE/DOCKET NUMBER: 1483.0140001
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 202-371-2540
12     TELEFAX: 202-371-2540
13     INFORMATION FOR SEQ ID NO: 2:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 579 base pairs
16     TYPE: nucleic acid
17     STRANDEDNESS: both
18     TOPOLOGY: both
19     MOLECULE TYPE: cDNA
20
21     US-08-798-897-2

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Query Match	89.2%	Score 518.2;	DB 1;	Length 579;
Best Local Similarity	93.4%;	Pred. No. 3.8e-133;		
Matches 541;	Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;

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QY	361	CAAGTGA	CAG	AG	AT	TGA	TG	TG	GC	CT	TA	CC	TG	GA	GA	CA	420
Db	361	CAAGTGA	CAG	AG	AT	TGA	TG	TG	GC	CT	TA	CC	TG	GA	GA	CA	420
QY	421	AGTGGG	GGCT	TGG	CC	GAG	TT	CA	AG	CT	TA	T	AC	GG	GG	A	480
Db	421	AGTGGG	GGCT	TGG	CC	GAG	TT	CA	AG	CT	TA	T	AC	GG	GG	A	480
QY	481	CGTCTG	CGG	AG	GG	GA	CT	GG	CA	T	CA	GT	GA	GA	CA	GT	540
Db	481	CGTCTG	CGG	AG	GG	GA	CT	GG	CA	T	CA	GT	GA	GA	CA	GT	540
QY	541	GGGGCC	CTG	T	A	CT	GT	A	GG	GC	CTTT	TT	T	G	CT	A	600
Db	541	GGGGCC	CTG	T	A	CT	GT	A	GG	GC	CTTT	TT	T	G	CT	A	600

RESULT 4  
US-08-978-523--2  
Sequence 2, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guatella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

1 TITLE OF INVENTION: Homologue  
2  
3 NUMBER OF SEQUENCES: 53  
4  
5 CORRESPONDENCE ADDRESS:  
6  
7 ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
8  
9 STREET: 1100 New York Avenue, N.W., Suite 600  
10  
11 CITY: Washington  
12  
13 STATE: DC  
14  
15 COUNTRY: USA  
16  
17 ZIP: 20005  
18  
19  
20 COMPUTER READABLE FORM:  
21  
22 MEDIUM TYPE: Floppy disk  
23  
24 COMPUTER: IBM PC compatible  
25  
26 OPERATING SYSTEM: PC-DOS/MS-DOS  
27  
28 SOFTWARE: Patent In Release #1.0, Version #1.30  
29  
30 CURRENT APPLICATION DATA:  
31  
32 APPLICATION NUMBER: US/08/978,523  
33  
34 FILING DATE: herewith  
35  
36 CLASSIFICATION: 424  
37  
38 PRIOR APPLICATION DATA:  
39  
40 APPLICATION NUMBER: US 08/796,897  
41  
42 FILING DATE: February 11, 1997  
43  
44 CLASSIFICATION: 424  
45  
46 ATTORNEY/AGENT INFORMATION:  
47  
48 NAME: Esmond, Robert W.  
49  
50 REGISTRATION NUMBER: 32,893  
51  
52 REFERENCE/DOCKET NUMBER: 1483.0140002  
53  
54 TELECOMMUNICATION INFORMATION:  
55  
56 TELEPHONE: 202-371-2600  
57  
58 TELEFAX: 202-371-2540  
59  
60 INFORMATION FOR SEQ ID NO: 2:  
61  
62 SEQUENCE CHARACTERISTICS:  
63  
64 LENGTH: 579 base pairs  
65  
66 TYPE: nucleic acid  
67  
68 STRANDEDNESS: both  
69  
70 TOPOLOGY: both  
71  
72 MOLECULE TYPE: CDNA  
73  
74  
75 US-08-978-523-2

Query Match	89.2%	Score 518.2;	DB 2;	Length 579;
Best Local Similarity	93.4%;	Pred. NO. 3.8e-133;		
Matches 541; Conservative	0;	Mismatches 38;	Indels 0;	Gaps 0;

QY	1	ATGGGACCCCGAGCTTCACC	CCACACACACGGGCTCTAGTGGCTGACCTTTGATGGCTAT	60
Db	1	ATGGGACCCCGAGCTTCGGG	CCCCCAACACACAGGGGCTCTGTGGAAAGACTTTGTAGTTAT	60
QY	61	AAGCTGAGGACGAAAGGTTATGTCTGTGAGCTGGCCCTTGGGGAAAGGCCACGCCGAC	120	
Db	61	AAGCTGAGGACGAAAGGTTATGTCTGTGAGCTGGCCCCCGGGAGAGGCCACACAGCTGAC	120	
QY	121	CCGCTGCACCAAGCCATGCGGGCTGTCTGGAGACGAGTTTGAACCCGTTTCCGCGGCAC	180	
Db	121	CCACTGCACCAAGCCATCGGGGACCTGGAGATGAGTTTGAACCCGCTTCCGCGGCAC	180	
QY	181	TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCACGACGACTTCACC	240	
Db	181	TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGGCTTCAC	240	
QY	241	CAGGTTTCCGACGAATCTTTCCAGAGGGGGCCCTAATCTGGGGCCGCTTGTGGCATTTCTT	300	
Db	241	CAGGCTCTCCGATGAACTTTTTCMAAGGGGGCCCCCACTGGGGCCGCCCTTGTAGCTTCTT	300	
QY	301	GTCTTTGGGGCGCCCTGTGTGCTGAGAGTGTCAACAAAGAATGGAGCTTTGTGGGGA	360	
Db	301	GTTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAAGAAATGGAAACCATCTGTGGGA	360	
QY	361	CAAGTGACAGATTGGATGATGGCTTACCTTGAGAGACAGTCTTGCTGACTGGATCCACAG	420	
Db	361	CAAGTGACAGAGTGGATGATGGCTTACCTTGAGAGACGCGGCTGGCTGACTGGATCCACAG	420	
QY	421	AGTGGGGGCTGGGCGGAGTTCAACACTCTATCTAGGGGAAAGGGGGCCTTGAAGAGGACGG	480	
Db	421	AGTGGGGGCTGGGCGGAGTTCAACACTCTATACGGGAAAGGGGGCCTTGAAGAGAGCGGG	480	

QY 481 CGTCTGCGGAGGAGGAACTGGGCATCAGTGAAGACAGTCTGACGCGGGCCGTGGCACATG 540  
DB 481 CCTCTGCGGAGGAGGAACTGGGCATCAGTGAAGACAGTCTGACGCGGGCCGTGGCACATG 540  
QY 541 GGGGCCCTGTGTAAGTGTAGGGCCCTTTTGTGTAGCAAG 579  
DB 541 GGGGCCCTGTGTAAGTGTAGGGCCCTTTTGTGTAGCAAG 579

## RESULT 5

US-09-010-147B-23  
Sequence 23, Application US/09010147B  
Patent No. 6653445

## GENERAL INFORMATION:

APPLICANT: Nt et al.  
TITLE OF INVENTION: Human Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC

## compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-NO. 6653445-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997

## ATTORNEY/AGENT INFORMATION:

NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8439  
TELEFAX: 301-309-8504

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1098 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
FEATURE:

NAME/KEY: CDS  
LOCATION: 1..1095

SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-010-147B-23

Query Match 64.7%; Score 376; DB 4; Length 1098;  
Best Local Similarity 91.9%; Pred. No. 5.5e-94;  
Matches 397; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTCAACCCAGACACACAGGAGCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGGACCCCAAGCTCAACCCAGACACACAGGAGCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAAGCCGCGAC 120  
DB 61 AAGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCGCGGGAAGGCCCAAGAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGGGGCTGTGAGAGAGAGTTGAGACCCGTTTCCGCGGACAC 180

DB 121 CCGCTGACCAAGCCATGGGGCTGTGAGAGAGAGTTGAGACCCGTTTCCGCGGACAC 180  
QY 121 TTCCTGACCTGGGCGGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
DB 121 TTCCTGACCTGGGCGGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
QY 241 CAGGTTCCGAGCAAGCTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTCCGAGCAAGCTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
QY 301 GTCTTTGGGCGCTGCTGCTGTGCTGAGAGTGTCAAAGAAATGAGACCTTTGGTGGGA 360  
DB 301 GTCTTTGGGCGCTGCTGCTGTGCTGAGAGTGTCAAAGAAATGAGACCTTTGGTGGGA 360  
QY 361 CAAGTGCAGAGTGGATGTGGCTTAAGTGAAGACAGCTGGGCTGACTGATCCAGAC 420  
DB 361 CAAGTGCAGAGTGGATGTGGCTTAAGTGAAGACAGCTGGGCTGACTGATCCAGAC 420  
QY 421 AGTGGGGGCTGG 432  
DB 421 AGTGGGGGCTGG 432

## RESULT 6

US-09-149-476-130  
Sequence 130, Application US/09149476  
Patent No. 6420526

## GENERAL INFORMATION:

APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
FILING DATE: 1998-09-08  
APPLICATION NUMBER: PCT/US98/04493  
FILING DATE: 1998-03-06  
APPLICATION NUMBER: 60/040,162  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/040,333  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/038,621  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/040,626  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/040,334  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/040,336  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/040,163  
FILING DATE: 1997-03-07  
APPLICATION NUMBER: 60/047,600  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,615  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,597  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,502  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,633  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,583  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,617  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,618  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,503  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,592  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,581  
FILING DATE: 1997-05-23  
APPLICATION NUMBER: 60/047,584



1	EARLIER APPLICATION NUMBER: 60/056,880
2	EARLIER FILING DATE: 1997-08-22
3	EARLIER APPLICATION NUMBER: 60/056,894
4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,911
6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,636
8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,874
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,910
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,845
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,992
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/057,761
18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/047,555
20	EARLIER FILING DATE: 1997-05-23
21	EARLIER APPLICATION NUMBER: 60/047,559
22	EARLIER FILING DATE: 1997-05-23
23	EARLIER APPLICATION NUMBER: 60/047,568
24	EARLIER FILING DATE: 1997-05-23
25	EARLIER APPLICATION NUMBER: 60/047,585
26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,586
28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,590
30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,594
32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,589
34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,593
36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,614
38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/043,578
40	EARLIER FILING DATE: 1997-04-11
41	EARLIER APPLICATION NUMBER: 60/043,576
42	EARLIER FILING DATE: 1997-04-11
43	EARLIER APPLICATION NUMBER: 60/047,501
44	EARLIER FILING DATE: 1997-05-23
45	EARLIER APPLICATION NUMBER: 60/043,670
46	EARLIER FILING DATE: 1997-04-11
47	EARLIER APPLICATION NUMBER: 60/056,632
48	EARLIER FILING DATE: 1997-08-22
49	EARLIER APPLICATION NUMBER: 60/056,664
50	EARLIER FILING DATE: 1997-08-22
51	EARLIER APPLICATION NUMBER: 60/056,876
52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/056,881
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,909
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,875
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056,862
60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056,887
62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056,908
64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/048,964
66	EARLIER FILING DATE: 1997-06-06
67	EARLIER APPLICATION NUMBER: 60/057,656
68	EARLIER FILING DATE: 1997-09-05
69	EARLIER APPLICATION NUMBER: 60/056,884

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 64.6%; Score 375.6; DB 4; Length 1864;  
Best Local Similarity 91.7%; Pred. No. 8,5e-94;  
Matches 396; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGAGCTCAACCCAGACACACAGGGCTCTAGTGGCTGATCTTTAGAGCTAT 60  
DB 11 ATGGGACCCCGAGCTCAACCCAGACACACAGGGCTCTAGTGGCTGATCTTTAGAGCTAT 70  
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCCGAC 120  
DB 71 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCGGAGAGGGCCAGACAGCTGAC 130  
QY 121 CCGCTGACACAGGACATGGGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGCAC 180  
DB 131 CCGCTGACACAGGACATGGGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGCAC 190  
QY 181 TTCTCTGACCTGCGCTCAGCTACACGTCAGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
DB 191 TTCTCTGATCTGCGGCTCAGCTGATGACCTCAAGGCTCAGCCCAACAGCTTCAAC 250  
QY 241 CAGGTTTCCAGCAACTTTTCCAGGGGGCCCTTAACCTGGGGCCGTTTGTGCAATTTCT 300  
DB 251 CAGGTTTCCAGCAACTTTTCCAGGGGGCCCTTAACCTGGGGCCGTTTGTGCAATTTCT 310  
QY 301 GCTTTGGGGGCTCCCTGTGTCTGAGATGTCAACAAAGAAATGAGCTTTGTGTGGA 360  
DB 311 GCTTTGGGGGCTCCCTGTGTCTGAGATGTCAACAAAGAAATGAGCTTTGTGTGGA 370  
QY 361 CAGATGACAGATGTGATGTGCTGACCTACCTGAGACACAGCTGCTGATGATCCACAGC 420  
DB 371 CAGATGACAGATGTGATGTGCTGACCTACCTGAGACACAGCTGCTGATGATCCACAGC 430  
QY 421 AGTGGGGGCTGG 432  
DB 431 AGTGGGGGCTGG 442

RESULT 7  
US-08-081-448-5  
Sequence 5, Application US/08081448  
Patent No. 5646008

GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.  
APPLICANT: Boise, Lawrence H.  
TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
TITLE OF INVENTION: Compositions and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee  
STREET: 321 No. 5646008th Clark Street, Suite 800  
CITY: Chicago

STATE: IL  
COUNTRY: USA  
ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/081,448  
FILING DATE: 19930622  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5646008thrup, Thomas E.

REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD090  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-744-0090  
TELEFAX: 312-755-4489

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 926 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

FEATURE:  
NAME/KEY: CDS  
LOCATION: 135..836

US-08-081-448-5

Query Match 22.9%; Score 133; DB 1; Length 926;  
Best Local Similarity 58.0%; Pred. No. 2.9e-27;  
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGCTCTGAGACGAGTTTGAGACCCGTTTCCGCGCACCTTCTCTG 187  
DB 394 AGCAAGCGCTGAGGAGGAGGAGCGAGGAGTTGAACTGGGTACCGGCGGCAATTCAGTG 453  
QY 188 ACCTGGCCGCTCAGCTACACGTCAGCCAGGCTCAGCCAGCAAGCTTCAACCCAGGTTT 247  
DB 454 ACTTGAATCTCCAGCTCAGCTACATCACCAGGAGCAGCATATCAGACTTTTGAACAGGTAG 513  
QY 248 CCGAGCACTTTTCCAGAGGGGCGCTTAACCTGGGGCCGTTTGTGCAATTTCTTTG 307  
DB 514 TGAATGAATCTTCCGAGGATGGGGTAACTGGGGTGGCATTTTCTTCTCTCG 573  
QY 308 GGGCTGCTGTGTCTGAGAGTGTCAACAAAGAAATGAGCTTTGTGTGGAACAAGTC 367  
DB 574 GCGGGGCACTGTGCTGAGAAAGCGTGAACAAAGAGATCAGATTTGTGTGAGTCGATCG 633  
QY 368 AGGATTGATGTGCTTACCTGAGACACGCTGCTGATGATCCACAGCAGTGGAG 427  
DB 634 CAGCTTGAATGACCACTTAACCTGAATGACCACTTAAGACCTTGAATCCAGAGAAAGGCG 693  
QY 428 GCTGGCCGAGATTCAACGCTCTATACGGGGAAGGGGCGCTTGAAGAGGACGCGCTTGC 487  
DB 694 GCTGGGATATCTTTGTGAACTCTATGGAACAATGACAGACGAGCGAAGAGGCGC 753  
QY 488 GGGAGGGAAGTGGGATCAGTGAAGACAGATGCTGACCGGGGCGC 532  
DB 754 AGGAACGCTTCAACCGCTGTCTCTGACGAGGCGCATGCTGTGCGC 798

RESULT 8  
US-08-470-670A-6  
Sequence 6, Application US/08470670A  
Patent No. 5834309

GENERAL INFORMATION:  
Patent No. 5834309 5710045

APPLICANT: Thompson, Craig B.  
APPLICANT: Boise, Lawrence H.  
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston

STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30



APPLICANT: Zhang, Qiongling  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0324  
CURRENT APPLICATION NUMBER: US/09/167,921A  
CURRENT FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (135)..(836)  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: L20121 Genbank  
DATABASE ENTRY DATE: 1994-07-26  
US-09-167-921-1

Query Match 22.9%; Score 133; DB 3; Length 926;  
Best Local Similarity 58.0%; Pred. No. 2.9e-27;  
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGAGACGAGTTTGAAGACCCGTTCCGCGCACCTTCTCTG 187  
DB 394 AGCAAGCCGTGAGGAGGAGGCGAGAGTTTGAAGTTGACCGGCGGCGCATTCAGTG 453  
QY 188 ACTGCGCCCTCAGTACACGTCGACCCCGCTCAGCCGACGACGACGCTTACCAGTTT 247  
DB 454 ACCTGACATCCGAGCTCCACATCACCCGAGGACGACATATCAGAGTTTGAACAGGTAG 513  
QY 248 CCGAGCACTTTCCAGAGGGGCGCTTAAGTGGGGCGCTTGTGGCATTTCTTGTCTTG 307  
DB 514 TGAATGAATCTTCCGCGGATGGGATTAAGTGGGCTTGTGGCTTTTCTCTTCTTG 573  
QY 308 GGGCTGCCCTGTGTGTGAGTGTCAACAAAGAAATGAGGCTTTGTGGAGCAAGTGC 367  
DB 574 GCGGGGCACTGTGCGTGAAGAGTGAACAGAGATGAGATTTGGTGAATCGGATCG 633  
QY 368 AGGATTGATGTGTGCGCTTACCTGAGACACGTTCTGCTGATCCACAGCATGGGG 427  
DB 634 CAGCTTGGATGCGCACTTACCTGAATGACCACTTGAAGCTTGTGATCCAGAGAACGGCG 693  
QY 428 GCTGGCGGAGTTCAAGCTTATACGGGGAGCGGGGCGCTGAGAGGACGCGCTTGC 487  
DB 694 GCTGGGATATCTTTTGTGAATCTTATGGGAAACAATGCAAGCAGCCGAAAGGCGC 753  
QY 488 GGGAGGGGAATGGGATCAGTGAAGACAGTGTGACGGGGCGG 532  
DB 754 AGGAAGCTTCAACCGCTGTTCTTGACCGGATGACTGTGGCGG 798

RESULT 11  
US-09-277-020-39  
Sequence 39, Application US/09277020  
Patent No. 6210892

GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation  
FILE REFERENCE: ISPH-0339  
CURRENT APPLICATION NUMBER: US/09/277,020  
CURRENT FILING DATE: 1999-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-277-020-39

Query Match 22.9%; Score 133; DB 3; Length 926;  
Best Local Similarity 58.0%; Pred. No. 2.9e-27;  
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTCTGTGAGACGAGTTTGAAGACCCGTTCCGCGCACCTTCTCTG 187  
DB 394 AGCAAGCCGTGAGGAGGAGGCGAGGAGTTTGAAGTTGACCGGCGGCGCATTCAGTG 453  
QY 188 ACTGCGCCCTCAGTACACGTTGACCCGAGCTCAGCCGACGACGCTTACCAGTTT 247  
DB 454 ACCTGACATCCGAGCTCCACATCACCCGAGGACGACATTCAGAGCTTTGAACAGGTAG 513  
QY 248 CCGAGCACTTTCCAGAGGGGCGCTTAAGTGGGGCGCTTGTGGCATTTCTTGTCTTG 307  
DB 514 TGAATGAATCTTCCGCGGATGGGATTAAGTGGGCTTGTGGCTTTTCTCTCTTG 573  
QY 308 GGGCTGCCCTGTGTCTGAGAGTGTCAACAAAGAAATGAGACCTTGTGTGGACAAAGTGC 367  
DB 574 GCGGGGCACTGTGCGTGAAGCCGTGAACAGGAGATCAGTATTTGTGAGTGGATCG 633  
QY 368 AGGATTGATGTGTGCTTACCTGAGACACGCTTGTGCTGATCCACAGCAGTGGAG 427  
DB 634 CAGCTTGAATGCGCACTTACCTGAATGACCACTTGAAGACCTTGAATCCAGAGAACGGCG 693  
QY 428 GCTGGCGGAGTTCAAGCTTATACGGGAGCGGGGCGCTTGAAGAGGACGCGCTTGC 487  
DB 694 GCTGGGATATCTTTTGTGAATCTTATGGGAAACAATGACAGCGGAGCGGAAAGGCGC 753  
QY 488 GGGAGGGAATGGGATCAGTGAAGACAGTGTGACGGGGCGG 532  
DB 754 AGGAAGCTTCAACCGCTGTTCTTGACGGGATGACTGTGGCGG 798

RESULT 12  
US-09-323-743-1  
Sequence 1, Application US/09323743  
Patent No. 6214986

GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qiongling  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0368  
CURRENT APPLICATION NUMBER: US/09/323,743  
CURRENT FILING DATE: 1999-06-01  
EARLIER APPLICATION NUMBER: 09/277,020  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (135)..(836)  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: L20121 Genbank  
DATABASE ENTRY DATE: 1994-07-26  
US-09-323-743-1

Query Match 22.9%; Score 133; DB 3; Length 926;  
Best Local Similarity 58.0%; Pred. No. 2.9e-27;  
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGAGACGAGTTTGAAGACCCGTTTCCGCGCACCTTCTCTG 187  
DB 394 AGCAAGCCGTGAGGAGGAGGCGAGGAGTTTGAAGTTGACCGGCGGCGCATTCAGTG 453

Qy 188 ACCTGGCCGCTCAGTACAGTGACCCAGGCTCAGCCCAAGCTTACCCAGGTTT 247  
Db 454 ACCTGACATCCAGCTCAGATCACCCAGGAGACGATATCAGAGCTTTAAACAGGTAG 513  
Qy 248 CCGAGCACTTTTCCAAAGGGGCCCCCTAATGCGGCGCCCTTGTGGCATTTCTTTG 307  
Db 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGGCGCATTTGTGCCCTTTTCTCTCG 573  
Qy 308 GGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGAGCAAGTGC 367  
Db 574 GCGGGGCACTGTGTGTGAGAAAGCGTAGCAAGAGATGCGATGTGTGATGCGATCG 633  
Qy 368 AGATTGGATGTGGCTTACCTGAGACAGCTGTGCTGATCGATCCAGACAGTGGGG 427  
Db 634 CAGCTTGATGGCCACTTACTGAAATGACACCTTAGACCTTTGATCCAGAGAAAGCGG 693  
Qy 428 GCTGGCGGAGTTGACAGCTCTATACGAGGAGACGGGGCCCTGAGAGGACAGCGCTTGC 487  
Db 694 GCTGGATACTTTTGTGAACTCTATGGGAACATGACAGCAGCGAGAGCCGAAAGGCGC 753  
Qy 488 GGGAGGGAACTGGGCACTCAGTAGAGACAGTGTGACGGGGCGG 532  
Db 754 AGGAACGCTTCAACCGCTGTGCTCTGACGGGCAATGATGTGCGG 798

## RESULT 13

US-08-461-511A-6  
Sequence 6, Application US/08461511A  
Patent No. 6303331

## GENERAL INFORMATION:

APPLICANT: Thompson, Craig B. B.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,511A

FILING DATE: 05-Jun-1995

CLASSIFICATION: UNKNOWN

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 926 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 135..836

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-08-461-511A-6  
Query Match 22.9%; Score 133; DB 4; Length 926;  
Best Local Similarity 58.0%; Pred. No. 2.9e-27;  
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Qy 128 ACCAAGCATCGGGCTGTGGAGACGAGTTTGAACCCGTTTCCGCGCACCTTCTTG 187  
Db 394 AGCAAGCGCTGAGGAGGACAGGCGACAGATTTTGAATGCGGTACCGCGGGCATTTCAAGT 453  
Qy 188 ACCTGGCCGCTCAGTACAGTGACCCAGGCTCAGCCAGCAAGCTTACCCAGGTTT 247  
Db 454 ACCTGACATCCAGCTCAGATCACCCAGGAGACGATATCAGAGCTTTAAACAGGTAG 513  
Qy 248 CCGAGCACTTTTCCAAAGGGGCCCCCTAATGCGGCGCCCTTGTGGCATTTCTTTG 307  
Db 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGGCGCATTTGTGCCCTTTTCTCTCG 573  
Qy 308 GGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGAGCAAGTGC 367  
Db 574 GCGGGGCACTGTGTGTGAGAAAGCGTAGCAAGAGATGCGATGTGTGATGCGATCG 633  
Qy 368 AGATTGGATGTGGCTTACCTGAGACAGCTGTGCTGATCGATCCAGACAGTGGGG 427  
Db 634 CAGCTTGATGGCCACTTACTGAAATGACACCTTAGACCTTTGATCCAGAGAAAGCGG 693  
Qy 428 GCTGGCGGAGTTGACAGCTCTATACGAGGAGACGGGGCCCTGAGAGGACAGCGCTTGC 487  
Db 694 GCTGGATACTTTTGTGAACTCTATGGGAACATGACAGCAGCGAGAGCCGAAAGGCGC 753  
Qy 488 GGGAGGGAACTGGGCACTCAGTAGAGACAGTGTGACGGGGCGG 532  
Db 754 AGGAACGCTTCAACCGCTGTGCTCTGACGGGCAATGATGTGCGG 798

## RESULT 14

US-09-271-014A-5  
Sequence 5, Application US/09271014A  
Patent No. 6395510

## GENERAL INFORMATION:

APPLICANT: THOMPSON, CRAIG B.

APPLICANT: BOISE, LAWRENCE H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS

FILE REFERENCE: ARCD:316

CURRENT APPLICATION NUMBER: US/09/271,014A

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 926

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: CDS

LOCATION: (135)..(836)

US-09-271-014A-5

Query Match 22.9%; Score 133; DB 4; Length 926;  
Best Local Similarity 58.0%; Pred. No. 2.9e-27;  
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;  
Qy 128 ACCAAGCATCGGGCTGTGGAGACGAGTTTGAACCCGTTTCCGCGCACCTTCTTG 187  
Db 394 AGCAAGCGCTGAGGAGGACAGGCGACAGATTTTGAATGCGGTACCGCGGGCATTTCAAGT 453  
Qy 188 ACCTGGCCGCTCAGTACAGTGACCCAGGCTCAGCCAGCAAGCTTACCCAGGTTT 247  
Db 454 ACCTGACATCCAGCTCAGATCACCCAGGAGACGATATCAGAGCTTTAAACAGGTAG 513  
Qy 248 CCGAGCACTTTTCCAAAGGGGCCCCCTAATGCGGCGCCCTTGTGGCATTTCTTTG 307  
Db 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGGCGCATTTGTGCCCTTTTCTCTCG 573  
Qy 308 GGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGAGCAAGTGC 367  
Db 574 GCGGGGCACTGTGTGTGAGAAAGCGTAGCAAGAGATGCGATGTGTGATGCGATCG 633  
Qy 368 AGATTGGATGTGGCTTACCTGAGACAGCTGTGCTGATCGATCCAGACAGTGGGG 427

Db 634 CAGCTTGATGGCCACTTACCTGATGACCACTAGAGCTTGATCCAGAGAACGGCG 693  
QY 428 GCTGGCCGAGCTTCACAGCTCTATACGGGAGACGGGCCCTGAGAGAGCAGCGCTTGC 487  
Db 694 GCTGGATATCTTTGTGAACTCTATGGACATGACAGCAGCCGAGAGCCGAAAGGCGC 753  
QY 488 GGGAGGGGAACCTGGCATCAGTGAAGACAGTGTGACGGGGCGG 532  
Db 754 AGGAACGCTTCAACCGCTGTTCTTGACGGGATATCTGTGCGG 798

## RESULT 15

US-09-023-655-1430  
Sequence 1430, Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1430:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 926 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9510900  
US-09-023-655-1430

Query Match 22.9%; Score 133; DB 4; Length 926;

Best Local Similarity 58.0%; Pred. No. 2.9e-27;

Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGCTGAGAGCACTTTGAGACCCGTTTCGCGCCGACCTTCTTG 187  
Db 394 ACCAAGCCGCTGAGGAGCGAGCGAGATTGAACTGCGGTACCGCGCGGATTCAGTG 453  
QY 188 ACTTGCCGCTCAGTCACTGACGTCACCGGCTCAGCCGACGCAAGCTTCAACCGAGTTT 247  
Db 454 ACTGACATCCAGCTCCACATCACCCGAGGAGCAGCATATCAGAGCTTTGAACAGGTAG 513

QY 248 CCGACGAATTTTCCAAAGGGGCCCTTAACGTGGGCGGTCTTGTGCAATTTCTTCTTG 307  
Db 514 TGAATGAACCTTCCGGGATGGGGTAACTGGGGTCCGATTTGTGCTTTCTTCTTG 573  
QY 308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGACAAAGTGC 367  
Db 574 GCGGGGCACTGTGTGCTGAAAGCGTAGCAAGAGATGCAAGTATTTGTTGAGTGGATCG 633  
QY 368 AGGATTGATGATGGCTTACCTGAGACACGCTGTGCTGATCTGATCCACAGCAGTGGGG 427  
Db 634 CAGCTTGATGAGCCACTTAACCTGAATGACACACTAGACCTTGGATCCAGAGAAAGCGCG 693  
QY 428 GCTGGCGGAGTTCAACAGCTTTATACGGGAGCGGGCCCTGAGAGGACAGCGCTTGC 487  
Db 694 GCTGGATATCTTTGTGAACTCTATGGGAACTATGCAAGATGACAGCCGAGCGGAAAGGCGC 753  
QY 488 GGGAGGGGAACCTGGCATCAGTGAAGACAGTGTCTGACGGGGCGG 532  
Db 754 AGGAACGCTTCAACCGCTGTTCTTGACGGGATATCTGTGCGG 798

Search completed: March 3, 2004, 18:38:47  
Job time : 87 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2004, 16:13:49 ; Search time 3188 seconds  
(without alignments)  
5442.261 Million cell updates/sec

Title: US-09-508-745-3

Perfect score: 581  
Sequence: 1 atggcgagccagcagctcaac.....gccttttctgctagcaagtg 581

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hc1:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc1:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estlum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_rhg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	582	29	AY421022 Mus muscu
2	581	100.0	1949	11	AK015644 Mus muscu
3	581	100.0	3487	11	AK004680 Mus muscu
4	579.4	99.7	969	13	BY715200 BY715200

5	524.4	90.3	967	13	BU503850
6	521.8	89.8	582	29	AY421020
7	498.4	85.8	804	9	AL157542
8	497.8	85.7	1030	10	BE793530
9	448.2	77.1	815	10	BF785386
10	433.8	74.7	697	12	B1770566
11	433	74.5	854	11	AK013244
12	420.2	72.3	792	12	BG298789
13	418.6	72.0	623	14	CB578463
14	414.8	71.4	540	10	AM258810
15	395	68.0	626	14	CA391923
16	370	63.7	643	12	B1910270
17	360	62.0	440	14	CB749817
18	354.8	61.1	559	13	BY704881
19	351.8	60.6	437	14	CB790932
20	342	58.9	548	14	CF533813
21	336.2	57.9	869	13	BU557268
22	336.2	57.9	872	13	BU557410
23	331.8	57.1	548	14	CA407899
24	330.2	56.8	645	13	BY740551
25	327	56.3	362	9	AA596919
26	314.8	54.2	410	14	CB804140
27	309.6	53.3	460	13	BY285647
28	304.4	52.4	449	13	BY253191
29	295.8	50.9	327	29	AY421021
30	295	50.8	1053	13	BU931540
31	288.4	49.6	758	12	B1764428
32	279	48.0	457	10	BB856021
33	275	47.3	430	14	CB760687
34	271.6	46.7	425	13	BY251598
35	268.6	46.2	467	13	BY253189
36	265.4	45.9	302	13	BY356166
37	263.8	45.4	305	13	BY356183
38	255.8	44.0	749	12	BG677345
39	254	43.7	353	13	BY312773
40	250	43.0	601	10	BF204905
41	248	42.7	375	13	BY302913
42	247.4	42.6	1054	13	BQ646339
43	246	42.3	372	13	BY133304
44	245.2	42.2	452	14	CB786193
45	244.8	42.1	314	13	BY356000

#### ALIGNMENTS

RESULT 1  
LOCUS AY421022  
DEFINITION Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY421022  
VERSION AY421022.1 GI:39776979  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence is made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source 1..582  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
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 /gene="BCL2L2"  
 /locus\_tag="HCM7418"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.4e-135;  
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGGACCCCGAGCTCAACCCACAGACACGCGGCTTGTAGTCTGACTTTGTAGGCTAT 60  
 1 ATGGGACCCCGAGCTCAACCCACAGACACGCGGCTTGTAGTCTGACTTTGTAGGCTAT 60  
 61 AAGCTGAGGACAGAGGGTTATGCTGTGAGCTGGCCCTGGGGAAGCCACGCCGAC 120  
 61 AAGCTGAGGACAGAGGGTTATGCTGTGAGCTGGCCCTGGGGAAGCCACGCCGAC 120  
 121 CCGCTGACCAACGACATGGCGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCAC 180  
 121 CCGCTGACCAACGACATGGCGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCAC 180  
 181 TTCTCTGACCTGGCGCTAGCTACACGTCGACCCAGGCTCAGCCAGCAAGCTTCAAC 240  
 181 TTCTCTGACCTGGCGCTAGCTACACGTCGACCCAGGCTCAGCCAGCAAGCTTCAAC 240  
 241 CAGGTTTCCGACAACTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGCAATTTCTT 300  
 241 CAGGTTTCCGACAACTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGCAATTTCTT 300  
 301 GCTTGTGGGCGCTGCGCTGTGTCTGAGATGTCACAAAGAAATGAGGCTTTGGTGGGA 360  
 301 GCTTGTGGGCGCTGCGCTGTGTCTGAGATGTCACAAAGAAATGAGGCTTTGGTGGGA 360  
 361 CAAAGTCAGAGATTGATGTGTGCTTCACTGAGACACGTCGCTGACTGTATCCACACG 420  
 361 CAAAGTCAGAGATTGATGTGTGCTTCACTGAGACACGTCGCTGACTGTATCCACACG 420  
 421 AAGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCGCTTGAGAGAGGACCG 480  
 421 AAGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCGCTTGAGAGAGGACCG 480  
 481 CGTCTGCGGAGAGGAGAACTGGGCACTGAGAGACAGTGTCTGACGGGGCGGTGGACATG 540  
 481 CGTCTGCGGAGAGGAGAACTGGGCACTGAGAGACAGTGTCTGACGGGGCGGTGGACATG 540  
 541 GGGGCGCTGTGTAAGTCTAGAGGCGCTTTTGTCTAGAGAAATG 581  
 541 GGGGCGCTGTGTAAGTCTAGAGGCGCTTTTGTCTAGAGAAATG 581

RESULT 2  
 AKO15644 1949 bp mRNA linear HTC 20-SEP-2003  
 LOCUS AKO15644  
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493048D08 product:Bcl2-like 2, full insert sequence.

ACCESSION AKO15644  
 VERSION AKO15644.1 GI:12854052  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

TITLE  
 JOURNAL MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaibuchi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawas, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL MEDLINE 20530913  
 PUBMED 11076861

REFERENCE 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

TITLE  
 JOURNAL MEDLINE 11076861

REFERENCE 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

TITLE  
 JOURNAL MEDLINE 11076861

REFERENCE 6  
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Furukawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Oka, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

TITLE  
 JOURNAL MEDLINE 11076861

REFERENCE 7  
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@res.gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse cDNAs. First strand cDNA was primed with a primer [5'] GAGAGAGAGATCCACAGAGCTTTTGTGTTTATVN 3'], cDNA was prepared by using triazole thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGATTCGAGTTAATTAATTAATTCACCCCGCCCGCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified plasmid vector KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI, 3'



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Location/Qualifiers  
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/clone="4930488D08"  
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Best Local Similarity 100.0%; Pred. No. 2,4e-135;  
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DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched  
library, clone:1200009124 product:Bcl2-like 2, full insert  
sequence.  
ACCESSION AK004680  
VERSION AK004680.1 GI:12836027  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Komno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishie, T., Harada, A.,  
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,  
Fujiwaka, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Matshiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861  
REFERENCE  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBMED 11076861  
REFERENCE  
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,  
Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,  
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,  
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Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,  
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,  
Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D.,  
Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,  
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,  
Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K.,  
Yoshino, M., Yamamatsu, M. and Hayashizaki, Y.  
TITLE Direct Submersion  
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for  
further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'] GAGAGAGAGAGCGCGCAGCTGAGTCTTTTCTTTTCTTCA 3'), cDNA was prepared by using triazole thio-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGAGAGAGTCCAGAGCTCACTTATTTATTTAAACCCCCCCC 3'). cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

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ORIGIN

Query Match 100.0%; Score 581; DB 11; Length 3487;  
Best Local Similarity 100.0%; Pred. No. 3.1e-135;  
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 GCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAGAAATGAGAGCTTGTG 360  
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361 CAAAGTCAGAGATTGATGTGTGCTTACCTGAGAGACAGCTGTGGCTGACTGATCCAC 420  
569 CAAAGTCAGAGATTGATGTGTGCTTACCTGAGAGACAGCTGTGGCTGACTGATCCAC 628

421 AGTGGGGCTGGCGGAGATTCAAGCTTATACGGGAGCGGGCCCTGGAGAGGACACG 480  
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689 GCTTGGCGGAGAGGAACTGGGCACTCACTGAGAGACAGTCTGACCGGGCCCTGGCACTG 748  
541 GGGGCGCTGGTAACTGATGAGGGCGCTTTTGTGCTAGCAAGT 581  
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RESULT 4

LOCUS BY15200 969 bp mRNA linear EST 17-DEC-2002  
DEFINITION BY15200 RIKEN full-length enriched, adult male testis Mus musculus  
CDNA clone 4930488D08 5', mRNA sequence.  
ACCESSION BY15200  
VERSION BY15200.1 GI:27128317  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamataka, T.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,  
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,  
Bacalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,  
Chotia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,  
Fletcher, C. F., Forrester, A., Frizet, K. S., Gascard, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
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Arikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, E. S.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
JOURNAL  
MEDLINE  
PUBMED  
22354683  
1246851

TITLE

COMMENT

Yoshihide Hayashizaki  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp/  
URL: http://genome-gsc.riken.go.jp/  
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P.,  
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
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DB 190 AAGTGAAGGCAAGAGGTTATGTCTGTGAGCTGGCCCTGGGGAGAGCCCAAGCCCGAC 249  
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QY 478 CCGCTCTGCGGAGGAGGAACTGGGCTATGATGAGAGACAGTCTGAC-GGGGCGCTGG 536  
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DEFINITION genomic survey sequence.  
ACCESSION AY421020  
VERSION AY421020.1 GI:39776977  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Clark A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 582)  
Clark A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.D.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS 2 (bases 1 to 582)  
Clark A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.D.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence as made by sequencing genomic exons and ordering them  
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VERSION AL157542.1 GI:7057943  
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SOURCE Homo sapiens (human)  
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AUTHORS Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
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Anorge, W., Winkler, U., Mewes, W., Well, B. and Wiemann, S.  
EST (Anorge, W., Winkler, U., Mewes, H.W., Well, B. and Wiemann, S.)  
Unpublished (1999)  
CONTACT: MIPS

MIPS  
Institut fuer Landstr. 1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert.  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
sequenced by EMBL European Molecular Biology Laboratories,  
Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.  
No sl sequence available.  
This clone (DKFZp761D0816) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

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Qy 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCT 300
Db 374 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCT 433
Qy 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGGT 360
Db 434 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGGT 493
Qy 361 CAAGTGACAGATTGATGTGAGCTTACTCTGAGACACGCTGCTGACTGATCCACAG 420
Db 494 CAAGTGACAGATTGATGTGAGCTTACTCTGAGACACGCTGCTGACTGATCCACAG 553
Qy 421 AGTGGGGGCTGGGCGGAGTTCAACGCTTATACGGGGACGGGGCGCTGAGAGGAC 480
Db 554 AGTGGGGGCTGGGCGGAGTTCAACGCTTATACGGGGACGGGGCGCTGAGAGGAC 612
Qy 481 CGTCTGCGGGAGGGGAACTGGGGCACTAGTGAAGGACAGTGTGACGGGGCGCTG 540
Db 613 CGTCTGCGGGAGGGGAACTGGGGCACTAGTGAAGGACAGTGTGACGGGGCGCTG 671
Qy 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581
Db 672 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 712
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RESULT 8  
LOCUS BE793530  
DEFINITION BE793530 1030 bp mRNA linear EST 20-SEP-2000  
ACCESSION BE793530  
VERSION BE793530.1 GI:10214832  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1030)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
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High quality sequence start: 5  
High quality sequence stop: 709.

FEATURES  
source

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/clone="IMAGE:3944307"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="MDH10B (phage-resistant)"
/clone_lib="NIH-MGC_7"
/note="Organ: Lung; Vector: pOTB7; Site_1: XhoI; Site_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using Zap-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

Query Match 85.7%; Score 497.8; DB 10; Length 1030;  
Best Local Similarity 91.0%; Pred. No. 1.7e-114;  
Matches 529; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 60
Db 144 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 203
Qy 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGCCCGAC 120
Db 204 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGACACTGAC 263
Qy 121 CCGCTGACCAAGCCATCGGGGCTGCTGAGACAGAGTTTGAAGACCGCTTCCGGCAG 180
Db 264 CCGCTGACCAAGCCATCGGGGCTGCTGAGACAGAGTTTGAAGACCGCTTCCGGCAG 323
Qy 181 TTCTCTGACTGGCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTAC 240
Db 324 TTCTCTGACTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTAC 383
Qy 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCT 300
Db 384 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCT 443
Qy 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGGT 360
Db 444 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGGT 503
Qy 421 AAGTGGGGCTGGGCGGAGTTCAACGCTTATACGGGACGGGGCGCTTGGAGAGGAC 480
Db 504 AAGTGGGGCTGGGCGGAGTTCAACGCTTATACGGGACGGGGCGCTTGGAGAGGAC 563
Qy 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581
Db 564 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 623
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QY 481 CCGTCGCGGAGGAGAACTGGGCAATGAGAGACAGTGTGACGCGGGCCGTGGCACTG 540  
DB 624 CGTCTGCGGGGAGGAGGAGCTGGGCAATGAGAGACAGTGTGACGCGGGCCGTGGCACTG 683  
QY 541 GGGGCCCTGTGACTGTAGAGGGCCCTTTTGTGCTAGCAAGT 581  
DB 684 GGGGGCCCTGTGACTGTAGAGGGCCCTTTTGTGCTAGCAAGT 724

RESULT 9  
BF785386 815 bp mRNA linear EST 12-JAN-2001  
LOCUS 602111728P1 NCI CGAP\_Kid14 Mus musculus cDNA clone IMAGE:4239798  
DEFINITION 5', mRNA sequence.  
ACCESSION BF785386.1 GI:12090422  
VERSION BF785386.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 815)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM9853 row: h column: 07  
High quality sequence start: 3  
High quality sequence stop: 650.  
Location/Qualifiers  
1..815  
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/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4239798"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP\_Kid14"  
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP Library."

ORIGIN  
Query Match 77.1%; Score 448.2; DB 10; Length 815;  
Best Local Similarity 96.9%; Pred. No. 4.8e-102;  
Matches 532; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

QY 21 CCCAACAACACGGGCTCTAGTGGCTGACTTTTGAAGCTTAAGCAGCAGCAAGGCTTA 80  
DB 2 CCCAACAACACGGGCTCTAGTGGCTGACTTTTGAAGCTTAAGCAGCAGCAAGGCTTA 60  
QY 81 TGTCTGTGAGCTGGGCTGGGAGAGGCCACCGCCGACCGCTGACCAACCAAGCATGG 140  
DB 61 TGTCTGTGAGCTGGGCTGGGAGAGGCCACCGCCGACCGCTGACCAACCAAGCATGG 120  
QY 141 GCGTGTGAGAGCAGATTGAGACCGGTTCCGCGCACCTTCTGACTGGCGGCTCA 200  
DB 121 GCGTGTGAGAGCAG- TTGAGACCGGTTCCGCGCACCTTCTGACTGGCGGCTCA 179  
QY 201 GCTACACGTGACCCCAAGGCTCAGCCAGCAAGCTTCAACCAAGGTTTCCGAGCAACTTT 260  
DB 180 GCTACACGTGACCCCAAGGCTCAGCCAGCAAGCTTCAACCAAGGTTTCCGAGCAACTTT 239  
QY 261 CCAAGGGGCGCTTAAGTGGGCGCTTGTGATTTGGGGCTGGCCCTGTG 320

DB 240 CCAAGGGGCGCTTAAGTGGGCGCTTGTGATTTGGGGCTGGCCCTGTG 296  
QY 321 TGTCTGTGAGCTGGGCTGGGAGAGGCCACCGCCGACCGCTGACCAACCAAGCATGG 380  
DB 297 TGTCTGTGAGCTGGGCTGGGAGAGGCCACCGCCGACCGCTGACCAACCAAGCATGG 355  
QY 381 GCGCTACCTGAGACACGCTGTGCTGACTGTGATCCACAGCAGTGGGGGCTGGGCGAGTT 440  
DB 356 GCGCTACCTGAGACACGCTGTGCTGACTGTGATCCACAGCAGTGGGGGCTGGGCGAGTT 415  
QY 441 CACAGCTTATTCGGGGACGGGGCCCTTGGAGAGGACAGCGCTCTGCGGAGGGAACTG 500  
DB 416 CACAGCTTATTCGGGGACGGGGCCCTTGGAGAGGACAGG- GTCTGCGGAGGGGAAAC-G 473  
QY 501 GGCATCAGTGAAGGACAGTGTGACGGGGGCGGTGACCTGGGGGCGCTGTACTGTAGG 560  
DB 474 GGCATCAGTGAAGGACAGTGTGACGGGGGCGGTGACCT- GGGGGCGCTGTACTGTAGG 532  
QY 561 GGCCTTTT 569  
DB 533 GGCCTTTT 541

RESULT 10  
B1770566 697 bp mRNA linear EST 25-SEP-2001  
LOCUS 601060362P1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:55209862 5',  
DEFINITION mRNA sequence.  
ACCESSION B1770566.1 GI:15762144  
VERSION B1770566  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 697)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM11526 row: k column: 15  
High quality sequence start: 21  
High quality sequence stop: 695.  
Location/Qualifiers  
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/clone="IMAGE:55209862"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_122"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH\_MGC Library."

ORIGIN  
Query Match 74.7%; Score 433.8; DB 12; Length 697;





(MGD|MG1:108052)  
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 LHGTGIPLMGMCAGRC"

## ORIGIN

Query Match 74.5%; Score 433; DB 11; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-98;  
 Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGGACCCCAAGCTTCAACCCCAAGACAGAGGCTCTAGTGTGACTTTTATAGCTAT 60  
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 196 ATGGGACCCCAAGCTTCAACCCCAAGACAGAGGCTCTAGTGTGACTTTTATAGCTAT 255  
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 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120  
 |||||  
 256 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 315  
 |||||  
 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGAGAGTTTGAAGACCCGTTCCGCGCAC 180  
 |||||  
 316 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGAGAGTTTGAAGACCCGTTCCGCGCAC 375  
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 181 TTCTGTACCTGCGCGCTCACTACAGTACAGTACCCCAAGGCTCAAGCCAGACAGCTTAC 240  
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 376 TTCTGTACCTGCGCGCTCACTACAGTACAGTACCCCAAGGCTCAAGCCAGACAGCTTAC 435  
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 241 CAGGTTTCCGAGGAACTTTTCAAGGGGGCCCTTAAGTGGGGCGCTTGTGACTTTCTT 300  
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 436 CAGGTTTCCGAGGAACTTTTCAAGGGGGCCCTTAAGTGGGGCGCTTGTGACTTTCTT 495  
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 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA 360  
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 496 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA 555  
 |||||  
 361 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGAGACAGTGTGCTGACTGTGATCCACAGC 420  
 |||||  
 556 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGAGACAGTGTGCTGACTGTGATCCACAGC 615  
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 421 AGTGGGGGCTGGG 433  
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 616 AGTGGGGGCTGGG 628

RESULT 12  
 BG298789 792 bp mRNA linear EST 21-FEB-2001  
 LOCUS 602396527F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4511215 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG298789  
 VERSION BG298789.1 GI:13063794  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 792)  
 NIH-MGC http://mgc.ncl.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: The Cepco Laboratories, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LIML at:  
 http://image.liml.gov

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 High quality sequence stop: 713.  
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 /clone="IMAGE:4511215"  
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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: pCMV-SORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## FEATURES

## source

## ORIGIN

Query Match 72.3%; Score 420.2; DB 12; Length 792;  
 Best Local Similarity 99.1%; Pred. No. 5.4e-95;  
 Matches 433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1 ATGGGACCCCAAGCTTCAACCCCAAGACAGAGGCTCTAGTGTGACTTTTATAGCTAT 60  
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 99 ATGGGACCCCAAGCTTCAACCCCAAGACAGAGGCTCTAGTGTGACTTTTATAGCTAT 158  
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 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120  
 |||||  
 159 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 218  
 |||||  
 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGAGAGTTTGAAGACCCGTTCCGCGCAC 180  
 |||||  
 219 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGAGAGTTTGAAGACCCGTTCCGCGCAC 278  
 |||||  
 181 TTCTGTACCTGCGCGCTCACTACAGTACAGTACCCCAAGGCTCAAGCCAGACAGCTTAC 240  
 |||||  
 279 TTCTGTACCTGCGCGCTCACTACAGTACAGTACCCCAAGGCTCAAGCCAGACAGCTTAC 337  
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 241 CAGGTTTCCGAGGAACTTTTCAAGGGGGCCCTTAAGTGGGGCGCTTGTGACTTTCTT 300  
 |||||  
 338 CAGGTTTCCGAGGAACTTTTCAAGGGGGCCCTTAAGTGGGGCGCTTGTGACTTTCTT 397  
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 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA 360  
 |||||  
 398 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA 457  
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 361 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGAGACAGTGTGCTGACTGTGATCCACAGC 420  
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 458 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGAGACAGTGTGCTGACTGTGATCCACAGC 517  
 |||||  
 421 AGTGGGGGCTGGG 437  
 |||||  
 518 AGTGGGGGCTGGTAAGA 534

RESULT 13  
 CS578463 623 bp mRNA linear EST 03-APR-2003  
 LOCUS CS578463  
 DEFINITION AMGNNUC:NRDGL-00100-H10-A nrdgl (10855) Rattus norvegicus cDNA  
 clone nrdgl-00100-h10 5', mRNA sequence.  
 ACCESSION CS578463  
 VERSION CS578463.1 GI:29522504  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE  
 AUTHORS Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick



Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00100 row: h column: 10.  
Location/Qualifiers

## FEATURES

source

1..623  
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/db\_xref="taxon:10116"  
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/clone\_lib="nr01 (10855)"  
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dorsal root ganglia"

## ORIGIN

Query Match 72.0%; Score 418.6; DB 14; Length 623;  
Best Local Similarity 97.9%; Pred. No. 1.2e-94;  
Matches 424; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGAGCTAT 60  
Db 191 ATGGGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGAGCTAT 250  
Qy 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGGCCGACGCGAC 120  
Db 251 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGGCCGACGCGAC 310  
Qy 121 CCGCTGCACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAAGACCCGTTCCGCGCAC 180  
Db 311 CCGCTGCACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAAGACCCGTTCCGCGCAC 370  
Qy 181 TTCTCTGACTGGCGCTGACTGACTGACGTAACCCAGGCTGACCCAGCAACGCTTACC 240  
Db 371 TTCTCTGACTGGCGCTGACTGACTGACGTAACCCAGGCTGACCCAGCAACGCTTACC 430  
Qy 241 CAGGTTCCGAGCACTTTTCCAGGGGGCCCTAAGGGGGCCGCTGTGGCAATTCCTT 300  
Db 431 CAGGTTCCGAGCACTTTTCCAGGGGGCCCTAAGGGGGCCGCTGTGGCAATTCCTT 490  
Qy 301 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360  
Db 491 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 550  
Qy 361 CAAGTCAGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
Db 551 CAAGTCAGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 610  
Qy 421 AGTGGGGGCTGGG 433  
Db 611 AGTGGGGGCTGGG 623

RESULT 14  
AM258810 540 bp mRNA linear EST 23-DEC-1999  
LOCUS um74a02.y1 Sugano mouse kidney mRna Mus musculus cDNA clone  
DEFINITION IMAGE:2300906 5' similar to SW:BCLM\_MOUSE P70345 APOPTOSIS  
REGULATOR BCL-W. [2] SW:BCLM\_MOUSE ; mRNA sequence.  
ACCESSION AM258810  
VERSION AM258810.1 GI:6631791  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,  
Peterson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,  
Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.  
TITLE The WashU-NCI Mouse EST Project 1999

## JOURNAL COMMENT

Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:1009678

## FEATURES

source

Seq primer: custom primer used  
High quality sequence stop: 465.  
Location/Qualifiers

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/mol\_type="mRNA"  
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/dev\_stage="adult"  
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/clone\_lib="Sugano mouse kidney mRna"  
/note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII  
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was primed with an oligo (dT) primer  
[ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor (TGTGGGCTCACTGG), digested  
and cloned into distinct DraIII sites of the pME18S-FL3  
vector (5' site CACTGTGG, 3' site CACCATGG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTCTGCTCTTAAAGCTTGGC and 3' end  
primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match 71.4%; Score 414.8; DB 10; Length 540;  
Best Local Similarity 99.3%; Pred. No. 1e-93;  
Matches 427; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 ATGGGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGAGGCTAT 60  
Db 112 ATGGGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGAGGCTAT 171  
Qy 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGAGTGGCCCTGGGGAAAGGCCAGCCGCGAC 120  
Db 172 AAGCTGAGGAGGAGGTTATGTCTGTGAGAGTGGCCCTGGGGAAAGGCCAGCCGCGAC 231  
Qy 121 CCGCTGCACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAAGACCCGTTCCGCGCAC 180  
Db 232 CCGCTGCACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAAGACCCGTTCCGCGCAC 291  
Qy 181 TTCTCTGACTGGCGCTGACTGACTGACGTAACCCAGGCTGACCCAGCAACGCTTACC 240  
Db 292 TTCTCTGACTGGCGCTGACTGACTGACGTAACCCAGGCTGACCCAGCAACGCTTACC 351  
Qy 241 CAGGTTCCGAGCACTTTTCCAGGGGGCCCTAAGTGGGGCCCTTTTGGCAATTCCTT 300  
Db 352 CAGGTTCCGAGCACTTTTCCAGGGGGCCCTAAGTGGGGCCCTTTTGGCAATTCCTT 411  
Qy 301 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360  
Db 412 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 471  
Qy 361 CAAGTCAGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
Db 472 CAAGTCAGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 530  
Qy 421 AGTGGGGGCT 430  
Db 531 AGTGGGGGCT 540

RESULT 15  
CA391923  
LOCUS  
DEFINITION CA391923 626 bp mRNA linear EST 06-NOV-2002  
cs20c09.y1 Human Retinal pigment epithelium/choroid CDNA  
(Un-normalized, unamplified): cs Homo sapiens CDNA clone cs20c09  
5', mRNA sequence.  
ACCESSION CA391923.1 GI:24724221  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 626)  
Wistow,G., Bernstein,S.L., Wyal,M.K., Parris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NEIbank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
JOURNAL 22103460  
MEDLINE 12107410  
PUBMED  
COMMENT  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 20 row: c column: 09  
Seq primer: M13RP1 reverse primer (AB1).  
Location/Qualifiers  
1..626  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"  
/clone="cs20c09"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_1ib="Human Retinal pigment epithelium/choroid CDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned CDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the Superscript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>. The library code  
designation was cs. For this library, CDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

## FEATURES

source

## ORIGIN

Query Match 68.0%; Score 395; DB 14; Length 626;  
Best Local Similarity 92.0%; Pred No. 1,1e-88;  
Matches 416; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 1 ATGGCAGCCCAAGCCTCAACCCAGACACACAGGAGCTTAGTGAGCTGACTTTGTAGGCTAT 60  
DB 175 ATGGGAGACCCAGCCTCGGCCAGACACACAGGAGCTTAGTGAGCTGACTTTGTAGGCTAT 234  
QY 61 AAGCTGAGGACAGAGGCTTATGTCTGTGAGCTGGCCCTGGGAGAGCCAGCCGCGAC 120  
DB 235 AAGCTGAGGACAGAGGCTTATGTCTGTGAGCTGGCCCGGAGGAGCCAGAGCTGAC 294  
QY 121 CGGCTGACCAAGCCATGGGGGCTGTGAGACAGAGTTGAGACCCGCTTCCGCGCACCC 180

DB 295 CCGCTGACCAAGCCATGGGGGAGCTGAGAGTAGTTGAGAGCCCGCTTCGCGCGCACCC 354  
QY 181 TTCTGTAGCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCACAGAGCTTCACCC 240  
DB 355 TTCTGTAGTCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCACAGAGCTTCACCC 414  
QY 241 CAGGTTTCCGACGAACTTTCCAGAGGGGCTTACGAGGAGCCGCTTTGTGAGCTTCCTT 300  
DB 415 CAGGCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCGCTGTAGCCCTTCTTT 474  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360  
DB 475 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGAGATGAACCACTGTGGGA 534  
QY 361 CAAGTCAGAGATTGGATGTGAGCTTACCTTGAGAGACAGCTGTGCTGACTGATCCACAGC 420  
DB 535 CAAGTCAGAGATTGATGTGAGCTTACCTTGAGAGAGCGGGCTGGCTGACTGATCCACAGC 594  
QY 421 AGTGGGGGCTGGGCGGAGTTCCAGAGCTCTATA 452  
DB 595 AGTGGGGGCTGGGCGGAGTTCCAGAGCTCTATA 626

Search completed: March 3, 2004, 18:37:14  
Job time : 3197 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: February 26, 2004, 11:06:41; Search time 60 Seconds  
(without alignments)  
908.861 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009

Sequence: 1 MATPASTPDRALVADRVGY.....LTGAVALGALVTGAFRASK 193

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database: A\_Geneseq\_29Jan04:\*  
Listing first 45 summaries

1: Geneseqp19808:\*  
2: Geneseqp19908:\*  
3: Geneseqp20008:\*  
4: Geneseqp20018:\*  
5: Geneseqp20028:\*  
6: Geneseqp20038:\*  
7: Geneseqp20048:\*  
8: Geneseqp20058:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1009	100.0	193	2	AAV05531 Mouse Bcl
2	1005	99.6	193	2	AAW61391 Rat bcl-y
3	1005	99.6	193	2	AAW97391 The rat b
4	1000	99.1	192	2	AAW97393 Protein s
5	1000	99.1	193	2	AAV05530 Human Bcl
6	1000	99.1	193	7	ADDA6742 Human Bcl
7	995	98.6	193	2	AAW61392 Human bcl
8	995	98.6	193	2	AAW97392 The human
9	993	98.4	193	2	AAW36047 Human bcl
10	993	98.4	193	2	AAW05532 Human Bcl
11	990	98.1	192	2	AAW97394 Mammalian
12	967.5	95.9	192	2	AAV05533 Mouse Bcl
13	876	86.8	168	2	AAW36048 Mouse bcl
14	814.5	80.7	190	5	AAO18223 Human Bcl
15	759	75.2	365	2	AAW59884 Amino aci
16	759	75.2	365	5	ABG95556 Human nov
17	759	75.2	365	6	ABO34750 Fragment
18	432.5	42.9	411	4	AAU00219 Bcl-XL-DT
19	430.5	42.7	237	5	ABG78480 Wild type
20	428.5	42.5	233	4	AAW73303 Rat wild-
21	428.5	42.5	233	7	ADBE62921 Rat Prote
22	428.5	42.4	233	7	ADBE6291 Rat Prote
23	427.5	42.4	233	2	AAW68887 Human thy
24	427.5	42.4	233	2	AAW05821 Bcl-XL pr
25	427.5	42.4	233	2	AAW31530 Human ant

26	427.5	42.4	233	3	AAV69969 Human Bcl
27	427.5	42.4	233	3	AAW83223 Bcl-x pol
28	427.5	42.4	233	4	AAW50538 Human Bcl
29	427.5	42.4	233	4	AAW64262 Human Bcl
30	427.5	42.4	233	4	AAW47515 Protein e
31	427.5	42.4	233	7	ADBE62493 Human Pro
32	427.5	42.4	236	6	ABR83558 To1A-BCL
33	427.5	42.4	348	6	ABR83557 To1A-BCL
34	425	42.1	225	2	AAW19396 "Depreryl
35	424.5	42.1	233	4	AAW73304 Mutant ra
36	415.5	41.2	239	4	AAW64037 Human Bcl
37	414.5	41.1	152	6	AAW79760 Bcl-XL. 4
38	412	40.8	236	4	AAW35131 Murine Bc
39	412	40.8	236	5	AAW76554 Murine Bc
40	411.5	40.8	239	2	AAW87810 Human B
41	411.5	40.8	239	4	AAW35130 Human Bcl
42	411.5	40.8	239	4	AAW74127 Human bcl
43	411.5	40.8	239	5	ABG78479 Human Bcl
44	411.5	40.8	239	5	ABG78478 Human Bcl
45	411.5	40.8	239	5	AAW76553 Human Bcl

## ALIGNMENTS

RESULT 1	AAV05531	standard; protein; 193 AA.
ID	AAV05531	
XX	AAV05531	
AC	AAV05531	
DT	05-JUL-1999	(first entry)
XX		
DE	Mouse Bcl-w protein essential for spermatogenesis.	
XX		
KW	Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility; animal model.	
XX		
OS	Mus sp.	
XX		
PN	W09913710-A1.	
XX		
PD	25-MAR-1999.	
XX		
PF	16-SEP-1998;	98WO-AU000764.
XX		
PR	16-SEP-1997;	97AU-00009228.
XX		
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
XX		
PI	Cory S, Adams J, Print C, Gibson L, Koentgen F,	
XX		
DR	WPI: 1999-243890/20.	
XX		
PT	N-FSDB: AAX25133.	
XX		
PS	An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.	
XX		
PS	Claim 2; Page 35; 52pp; English.	
XX		
CC	The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals.	
CC	Methods are provided for inducing or reducing fertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene (see AAX25133-35) or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise	

CC Facilitating spermatogenesis in animals, or which can induce infertility  
 XX Sequence 193 AA;

Query Match 100.0%; Score 1009; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-102;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFETRRFRT 60  
 DB 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFETRRFRT 60  
 QY 61 FSDLAQLHVTPEGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 DB 61 FSDLAQLHVTPEGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 QY 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAASVRTLGAVAL 180  
 DB 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAASVRTLGAVAL 180  
 QY 181 GALVTVGAFPAASK 193  
 DB 181 GALVTVGAFPAASK 193

## RESULT 2

AAW61391  
 ID AAW61391 standard; protein; 193 AA.

XX AC AAW61391;  
 XX DT 02-OCT-1998 (first entry)  
 DE Rat bcl-2 protein.  
 XX bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
 OS Rattus sp.  
 XX US5789201-A.  
 XX PD 04-AUG-1998.  
 XX PF 11-FEB-1997; 97US-00798897.  
 XX PR 23-FEB-1996; 96US-0012201P.  
 XX PA (COCE-) COCENSYS INC.  
 XX PI Guastella J;  
 XX DR WPI, 1998-446079/38.  
 XX DR N-PSDB; AAV28333.  
 PT Nucleic acids encoding B-cell lymphoma-2 protein - useful for producing  
 PT recombinant protein for use in treating uncontrolled cell growth e.g.  
 PT cancers.  
 PS Example; Fig 3A; 27pp; English.

XX The mammalian bcl-2 protein is a member of the bcl-2 family, components  
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
 CC and the apoptosis blocking activity. bcl-2 falls in the apoptosis  
 CC activity category. The recombinant protein may be used to prevent  
 CC uncontrolled cell growth, either by its direct administration to  
 CC recombinant genetic constructs to increase its expression in vivo. Also,  
 CC antisense constructs can be used in disorders where prevention of cell  
 CC death is desired

XX Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;  
 Best Local Similarity 99.5%; Pred. No. 2e-101;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFETRRFRT 60  
 DB 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFETRRFRT 60  
 QY 61 FSDLAQLHVTPEGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 DB 61 FSDLAQLHVTPEGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 QY 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAASVRTLGAVAL 180  
 DB 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAASVRTLGAVAL 180  
 QY 181 GALVTVGAFPAASK 193  
 DB 181 GALVTVGAFPAASK 193

## RESULT 3

AAW97391  
 ID AAW97391 standard; protein; 193 AA.

XX AC AAW97391;  
 XX DT 20-MAY-1999 (first entry)  
 DE The rat bcl-2 protein.  
 XX Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 OS Rattus sp.  
 XX US5883229-A.  
 XX PD 16-MAR-1999.  
 XX PF 25-NOV-1997; 97US-00978523.  
 XX PR 23-FEB-1996; 96US-0012201P.  
 XX PR 11-FEB-1997; 97US-00798897.  
 XX PA (COCE-) COCENSYS INC.  
 XX PI Guastella J;  
 XX DR WPI, 1999-214150/18.  
 XX DR N-PSDB; AAX15945.  
 PT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful for  
 PT modulating programmed cell death.  
 PS Disclosure; Col 15-18; 26pp; English.

XX The present sequence represents rat bcl-2 protein (Rbcl-2). The  
 CC specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and  
 CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in  
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2  
 CC proteins may be used to treat conditions associated with a disruption of  
 CC the cell death pathway. If they act as cell death inhibitors, they may be  
 CC used in therapies to treat subjects suffering from: strokes, head trauma,  
 CC Alzheimer's Disease, neural and muscular degenerative diseases  
 CC (especially multiple sclerosis), myocardial infarction, vitally induced  
 CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
 CC - conditions where cells under go premature cell death as a result of  
 CC triggers which may or may not be apparent. They may also be used in this  
 CC way to develop cell lines which remain viable in culture for an extended

CC period. In contrast, if they act as cell death stimulators, Bcl-1-y and  
CC Bcl01-y may be used to treat conditions associated with prolonged cell  
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)  
CC and auto/hyperimmune diseases. They may also be used to cause cell death  
CC in, and hence control, parasites  
XX  
XX Sequence 193 AA:  
SQ

Query Match	99.6%	Score 1005;	DB 2;	Length 193;
Best Local Similarly	99.5%;	Pred. No. 2e-101;		
Matches 192; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Oy	I MATPASTPDRALVADVFVGKURQKGVCAGPEBGPAPDPLHQMRAAGDEFFETFRRT	600
Db	1 MATPASTPDRALVADVFVGKURQKGVCAGPEBGPAPDPLHQMRAAGDEFFETFRRT	600

QY 61 FSDLAQLHVTGSAQQRFTQVSDLEFQGGPNWGRVAFPFYFGALCAESVVKEMEPLVG 120

Db 61 FSDLAQLHVTGSAQQRFTQVSDLEFQGGPNWGRVAFPFYFGALCAESVVKEMEPLVG 120

Qy 121 QVQDMVAIETRLADWIIHSGGMAEFTALYGDGAEARRIREGNASVRYLTGAVALL 180

Db 121 QVQDMVAIETRLADWIIHSGGMAEFTALYGDGAEARRIREGNASVRYLTGAVALL 180

QY	181	GALVTVGAF	FASK	193
Db	181	GALVTVGAF	FASK	193

RESULT 4  
AAW97393  
ID AAW97393 standard; protein; 192 AA  
....

AC	AAW97393;
XX	
DT	20-MAY-1999 (first entry)
..	

DE XX KW	Protein sequence of the specification  Rat bcl-y protein; Rbcl-Y; human bcl-y mammalian cell death oncogene
----------------	--

KM Rat bcl-1 protein; Bcl-1; human bcl-1 protein Bcl-1; bcl-2 homologue  
KM Programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke  
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KM multiple sclerosis; myocardial infarction; vitally induced cell death;  
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KM premature cell death; cell death stimulator; prolonged cell life span;  
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite

OS	Unidentified.
XX	
PN	US5883229-A.
XX	

PD	16-MAR-1999.
XX	
PF	25-NOV-1997;
XX	

PR	23-FEB-1996;	96US-0012201P.
PR	11-FEB-1997;	97US-00798897.
XX		
PA	(COCE-) COGENEVS TWT	

XX Guastella J;  
PI  
XX  
DB WPT. 1999-214150/18

Novel bcl-2 homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.

PS Disclosure; Col 19-20; 26pp; English.

CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis)

CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated

CC with a disruption of the cell death pathway. If they act as cell death  
CC inhibitors, they may be used in therapies to treat subjects suffering  
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
CC degenerative diseases (especially multiple sclerosis), myocardial  
CC infarction, vitally induced cell death, aging, spinal cord injuries and  
CC amyotrophic lateral sclerosis- conditions where cells under go premature  
CC cell death as a result of triggers which may or may not be apparent. They  
CC may also be used in this way to develop cell lines which remain viable in  
CC culture for an extended period. In contrast, if they act as cell death  
CC stimulators, Rbcl-y and Hbccl-y may be used to treat conditions associated  
CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites

Query Match	99.1%	Score 1000;	DB 2;	length 192;
Best Local Similarity	99.5%;	Pred. No. 7.1e-101;		
Matches 191; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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        |||||
Db      1 ATPASTPDTALVADVGKLRQKGYCGAGPEGPPADPLHQMRAGGEFETRERTF 60

```

QY 62 SDLAQLHTPGSAQQRFTQVSDLEFGGNNWGRVAFVFGAALCAESVNNEMEPVLVG 121

Db 61 SDLAQLHTPGSAQQRFTQVSDLEFGGNNWGRVAFVFGAALCAESVNNEMEPVLVG 120

Db 121 VQDMVTYETRELDWIHSSGMAEFTALYGDGALEARRREGNNA SVRTVLTGAVALG 180

Db 181 ALVTVGAFASK 1922

RESULT 5  
AAY05530  
ID AAY05530 standard; protein; 193 AA  
vv

ID	AA05530	standard; protein; 193 Aa.
XX		
AC	AA05530;	
XX		
DT	05-JUL-1999	(first entry)
XX		
DE	Human Bcl-w protein essential for spermatogenesis.	

KW	Spermatogenesis
KW	animal model.
XX	

XX	WO9913710-A1.
PN	
XX	
FD	25 MAR 1999

XX	16-SEP-1998;	98WO-AU000764.
PF		
XX		
DD	16-SEP-1997	97AUT-000009239

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA  
PA  
XX  
PI Corv S. Adams T. Print C. Gibson L. Koent

XX WPI, 1999-243890/20.  
DR N-PSDB, AAX25132.  
XX

PT An animal model exhibiting reduced levels of a Bcl-2 protein and/or

XX  
PS Claim 2, Page 33; 52pp; English.  
XX  
CC The present sequence is human Bcl-2, a pro-survival member of the Bcl-2

CC family which is widely expressed and which is essential for  
CC spermatogenesis. The invention relates generally to a method of treatment  
CC and to an animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male animals.  
CC Methods are provided for the treatment of infertility, or for reducing  
CC fertility, by modulating spermatogenesis. An animal model carries a  
CC mutation in at least one allele of the human or murine bcl-w gene (see  
CC AAX5132-35) or in a gene associated with bcl-w. Such animals have  
CC disorganized seminiferous tubules and are substantially infertile, but  
CC possess no other major abnormalities as determined by histological  
CC examination. They can be used to screen for therapeutic molecules  
CC including genetic sequences capable of inducing, enhancing or otherwise  
CC facilitating spermatogenesis in animals, or which can induce infertility  
XX SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 2; Length 193;  
Best Local Similarity 99.0%; Pred. No. 7.1e-101;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGEGPADPLHQMRAGDEFETRRPRT 60  
DB 1 MATPASAPDTRALVADPFGYKLRQKGYCGAGPGEGPADPLHQMRAGDEFETRRPRT 60  
QY 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120  
DB 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120  
QY 121 QVQDMWVAVLETRLDWIHSSGMAEFTALYGDGALBEARRLRBGNMASVRTVLGAVALL 180  
DB 121 QVQDMWVAVLETRLDWIHSSGMAEFTALYGDGALBEARRLRBGNMASVRTVLGAVALL 180  
QY 181 GALVTGAFPFASK 193  
DB 181 GALVTGAFPFASK 193

RESULT 6  
ADD46742  
ID ADD46742 standard; protein; 193 AA.

XX ADD46742;  
AC 29-JAN-2004 (first entry)  
DT Human Protein Q92843, SEQ ID NO 12427.  
XX DE  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX OS Homo sapiens.  
XX PN WO2003016475-A2.  
XX PD 27-FEB-2003.  
XX PF 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
XX PR 01-NOV-2001; 2001US-0346382P.  
XX PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GHEO) GEN HOSPITAL CORP.  
XX PA (FARB) BAYER AG.  
XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX DR WPI; 2003-268312/26.  
XX DR GENBANK; Q92843.  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 7; Length 193;  
Best Local Similarity 99.0%; Pred. No. 7.1e-101;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGEGPADPLHQMRAGDEFETRRPRT 60  
DB 1 MATPASAPDTRALVADPFGYKLRQKGYCGAGPGEGPADPLHQMRAGDEFETRRPRT 60  
QY 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120  
DB 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120  
QY 121 QVQDMWVAVLETRLDWIHSSGMAEFTALYGDGALBEARRLRBGNMASVRTVLGAVALL 180  
DB 121 QVQDMWVAVLETRLDWIHSSGMAEFTALYGDGALBEARRLRBGNMASVRTVLGAVALL 180  
QY 181 GALVTGAFPFASK 193  
DB 181 GALVTGAFPFASK 193

RESULT 7  
AAM61392  
ID AAM61392 standard; protein; 193 AA.

XX AAM61392;  
AC 02-OCT-1998 (first entry)  
DT Human bcl-y protein.  
XX DE  
XX Human bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
XX OS Homo sapiens.  
XX PN US5789201-A.  
XX PN 04-AUG-1998.  
XX PD 11-FEB-1997; 97US-00798897.  
XX PF

```
XX 23-FEB-1996; 96US-0012201P.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI, 1998-446079/38.
XX N-PSDB; AAV28334.
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
XX recombinant protein for use in treating uncontrolled cell growth e.g.
XX cancers.
XX Example; Column 17/18; 27pp; English.
XX The mammalian bcl-Y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-Y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired
XX
SQ Sequence 193 AA;
Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.5e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASPTDTRALVADFGYGLRQKGYVCGAPGEGPAADPLHQAAMRAAGDEFETRRPRT 60
D 1 MATPASAPDTRALVEDFGYGLRQKGYVCGAPGEGPAADPLHQAAMRAAGDEFETRRPRT 60
QY 61 FSDLAQLHVTTPGSAQORFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
D 61 FSDLAQLHVTTPGSAQORFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
D 121 QVQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
QY 181 GALVTGAFPAK 193
D 181 GALVTGAFPAK 193
Db 181 GALVTGAFPAK 193
RESULT 8
AAW97392
ID AAW97392 standard; protein; 193 AA.
XX
AC AAW97392;
XX
DT 20-MAY-1999 (first entry)
XX
DE The human bcl-Y protein.
XX
KM Rat bcl-Y protein; Rbcl-Y; human bcl-Y protein; Hbcl-Y; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM premature cell death; cell death stimulator; prolonged cell life span;
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Homo sapiens.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
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XX 23-FEB-1996; 96US-0012201P.
XX 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI, 1999-214150/18.
XX N-PSDB; AAX15946.
XX Novel bcl-Y homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.
XX Claim 1; Col 17-18; 26pp; English.
XX
XX The present sequence represents human bcl-Y protein (Hbcl-Y). The
XX specification also describes rat bcl-Y protein (Rbcl-Y). Rbcl-Y and Hbcl-
XX Y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-Y and Hbcl-Y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended
XX period. In contrast, if they act as cell death stimulators, Rbcl-Y and
XX Hbcl-Y may be used to treat conditions associated with prolonged cell
XX life span such as cancer (especially kaposi's sarcoma and lung cancer)
XX and auto/hyperimmune diseases. They may also be used to cause cell death
XX in, and hence control, parasites
XX
SQ Sequence 193 AA;
Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.5e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASPTDTRALVADFGYGLRQKGYVCGAPGEGPAADPLHQAAMRAAGDEFETRRPRT 60
D 1 MATPASAPDTRALVEDFGYGLRQKGYVCGAPGEGPAADPLHQAAMRAAGDEFETRRPRT 60
QY 61 FSDLAQLHVTTPGSAQORFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
D 61 FSDLAQLHVTTPGSAQORFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
D 121 QVQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
QY 181 GALVTGAFPAK 193
D 181 GALVTGAFPAK 193
Db 181 GALVTGAFPAK 193
RESULT 9
AAW36047
ID AAW36047 standard; protein; 193 AA.
XX
AC AAW36047;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w protein.
XX
KM Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KM diagnosis; degenerative disease.
XX
OS Homo sapiens.
XX
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PN W09735971-A1.  
XX  
PD 02-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-AU000199.  
XX  
PR 27-MAR-1996; 96AU-00008965.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Cory S, Adams JM, Gibson LM, Holmgreen SP,  
XX  
DR WPI; 1997-489635/45.  
XX  
N-PSDB; AAT96577.  
XX  
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
XX  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
XX  
PS diseases.  
XX  
PS Claim 6; Page 48; 86pp; English.  
XX  
CC This sequence represents a novel human protein, bcl-w, encoded by the bcl  
XX  
CC -2 gene family and extracted from an adult brain library. This gene  
XX  
CC promotes cell survival, so its modulation is useful in treatment of  
XX  
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
XX  
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
XX  
CC ischaemia, human immunodeficiency virus infection or in cell transplants.  
XX  
CC Up-regulation of the gene can also be used to modify cell lines cultured  
XX  
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
XX  
CC and to increase survival of primary explants during genetic modification.  
XX  
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
XX  
CC antibody production or screening of potential modulators  
XX  
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;  
Best Local Similarity 97.9%; Pred. No. 4.2e-100;  
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
QY 61 FSDLAAGLHVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120  
DB 61 FSDLAAGLHVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120  
QY 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMA SVRTVLTGAVAL 180  
DB 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMA SVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 10

AAV05532  
ID AAV05532 standard; protein; 193 AA.

XX AC AAV05532;

XX DT 05-JUL-1999 (first entry)

XX DE Human Bcl-w protein essential for spermatogenesis.

XX KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
XX animal model.

XX OS Homo sapiens.

XX PN W09913710-A1.

PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU000764.  
XX  
PR 16-SEP-1997; 97AU-00009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX  
DR WPI; 1999-243890/20.  
XX  
N-PSDB; AAX25134.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
XX  
PT protein associated with Bcl-w.  
XX  
PS Disclosure; Page 37; 52pp; English.  
XX  
CC The present sequence is described of a derivative of human Bcl-w (see  
XX  
CC also AAV05530), a pro-survival member of the Bcl-2 family that is widely  
XX  
CC expressed and which is essential for spermatogenesis. The invention  
XX  
CC relates generally to a method of treatment and to an animal model for the  
XX  
CC identification of molecules and genetic sequences useful for inducing or  
XX  
CC reducing fertility of male animals. Methods are provided for the  
XX  
CC treatment of infertility, or for reducing fertility, by modulating  
XX  
CC spermatogenesis. An animal model carries a mutation is at least one  
XX  
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
XX  
CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
XX  
CC and are substantially infertile, but possess no other major abnormalities  
XX  
CC as determined by histological examination. They can be used to screen for  
XX  
CC therapeutic molecules including genetic sequences capable of inducing,  
XX  
CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
XX  
CC can induce infertility  
XX  
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;  
Best Local Similarity 97.9%; Pred. No. 4.2e-100;  
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
QY 61 FSDLAAGLHVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120  
DB 61 FSDLAAGLHVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120  
QY 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMA SVRTVLTGAVAL 180  
DB 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMA SVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 11

AAW97394  
ID AAW97394 standard; protein; 192 AA.

XX AC AAW97394;

XX DT 20-MAY-1999 (first entry)

XX DE Mammalian bcl-y protein.

XX KW Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;

XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
XX multiple sclerosis; myocardial infarction; vitally induced cell death;

XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
XX premature cell death; cell death stimulator; prolonged cell life span;



KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
XX Mammalia.  
XX US5883229-A.  
XX PD 16-MAR-1999.  
XX PE 25-NOV-1997; 97US-00978523.  
XX PR 23-FEB-1996; 96US-0012201P.  
XX PR 11-FEB-1997; 97US-00798897.  
XX PA (COCE-) COCENSYS INC.  
XX PI Guastella J;  
XX DR WPI; 1999-214150/18.  
XX PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
XX PT modulating programmed cell death.  
XX PS Claim 2; Col 19-22; 26pp; English.  
XX CC The present sequence represents a mammalian bcl-y protein. The  
XX CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
XX CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
XX CC thought to be involved in programmed cell death (apoptosis and necrosis).  
XX CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
XX CC with a disruption of the cell death pathway. If they act as cell death  
XX CC inhibitors, they may be used in therapies to treat subjects suffering  
XX CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
XX CC degenerative diseases (especially multiple sclerosis), myocardial  
XX CC infarction, vitally induced cell death, aging, spinal cord injuries and  
XX CC amyotrophic lateral sclerosis- conditions where cells under go premature  
XX CC cell death as a result of triggers which may or may not be apparent. They  
XX CC may also be used in this way to develop cell lines which remain viable in  
XX CC culture for an extended period. In contrast, if they act as cell death  
XX CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated  
XX CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
XX CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
XX CC cause cell death in, and hence control, parasites  
XX SQ Sequence 192 AA;  
SQ Query Match 98.1%; Score 990; DB 2; Length 192;  
Best Local Similarity 98.4%; Pred. No. 8.8e-100;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ATPASTPPTALVADFVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFFTRFRRTF 61  
DB 1 ATPASAPPTRALVDFVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFFTRFRRTF 60  
QY 62 SDLAOLHVTGSAQOQRTQVSDDELFOGPGNMGRLVAFVFGALCAESYNKMEPLVIG 121  
DB 61 SDLAOLHVTGSAQOQRTQVSDDELFOGPGNMGRLVAFVFGALCAESYNKMEPLVIG 120  
QY 122 VQDMVAVLETRLDWIMHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVALG 181  
DB 121 VQDMVAVLETRLDWIMHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVALG 180  
QY 182 ALVTVGAFPAK 193  
DB 181 ALVTVGAFPAK 192

RESULT 12  
AA05533  
ID AA05533 standard; protein; 192 AA.  
XX AC AA05533;  
XX DT 05-JUL-1999 (first entry)

XX DE Mouse Bcl-w protein derivative.  
XX KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
XX KW animal model.  
XX OS Mus sp.  
XX PN WO9913710-A1.  
XX PD 25-MAR-1999.  
XX PF 16-SEP-1998; 98WO-AU000764.  
XX PR 16-SEP-1997; 97AU-00009228.  
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX DR WPI; 1999-243890/20.  
XX DR N-PSDB; AAX25135.  
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
XX PT protein associated with Bcl-w.  
XX PS Disclosure; Page 39; 52pp; English.  
XX CC The present sequence is described of a derivative of mouse Bcl-w (see  
XX CC also AA05533), a pro-survival member of the Bcl-2 family that is widely  
XX CC expressed and which is essential for spermatogenesis. The derivative  
XX CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates  
XX CC generally to a method of treatment and to an animal model for the  
XX CC identification of molecules and genetic sequences useful for inducing or  
XX CC reducing fertility of male animals. Methods are provided for the  
XX CC treatment of infertility, or for reducing fertility, by modulating  
XX CC spermatogenesis. An animal model carries a mutation is at least one  
XX CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
XX CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
XX CC and are substantially infertile, but possess no other major abnormalities  
XX CC as determined by histological examination. They can be used to screen for  
XX CC therapeutic molecules including genetic sequences capable of inducing,  
XX CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
XX CC can induce infertility  
XX SQ Sequence 192 AA;  
SQ Query Match 95.9%; Score 967.5; DB 2; Length 192;  
Best Local Similarity 95.9%; Pred. No. 2.5e-97;  
Matches 185; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
QY 1 MATPASTPPTRALVADFVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFFTRFRRT 60  
DB 1 MPTASTPPTRALVADFVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFFTRFRRT 60  
QY 61 FSDLAOLHVTGSAQOQRTQVSDDELFOGPGNMGRLVAFVFGALCAESYNKMEPLVIG 120  
DB 61 FSDLAOLHVTGSAQOQRTQVSDDELFOGPGNMGRLVAFVFGALCAESYNKMEPLVIG 120  
QY 121 QVDMVAVLETRLDWIMHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVALG 180  
DB 121 QVDMVAVLETRLDWIMHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVALG 179  
QY 181 GALVTGAFPAK 193  
DB 180 GALVTGAFPAK 192

RESULT 13  
AAW36048  
ID AAW36048 standard; protein; 168 AA.  
XX AC AAW36048;

XX 22-APR-1998 (first entry)  
 XX Mouse bcl-w protein.  
 DE  
 XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 XX diagnosis; degenerative disease.  
 XX Mus sp.  
 OS  
 XX WO9735971-A1.  
 XX  
 XX 02-OCT-1997.  
 XX  
 XX 27-MAR-1997; 97WO-AU000199.  
 XX  
 XX 27-MAR-1996; 96AU-00008965.  
 XX  
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX  
 XX Cory S, Adams JM, Gibson LM, Holmgren SP;  
 PI  
 XX WPI; 1997-489635/45.  
 DR  
 XX N-PSDB; AAT96578.  
 XX  
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
 PT diseases.  
 XX  
 XX Claim 6; Page 50-51; 86pp; English.  
 XX  
 XX This sequence represents a novel protein, bcl-w, encoded by the mouse bcl  
 CC -2 gene family. This gene promotes cell survival, so its modulation is  
 CC useful in treatment of cancer or auto-immune diseases, degenerative  
 CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular  
 CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection  
 CC or in cell transplants. Up-regulation of the gene can also be used to  
 CC modify cell lines cultured in vivo, e.g. to develop new lines, to  
 CC facilitate isolation of hybridomas and to increase survival of primary  
 CC explants during genetic modification. It can be used to produce  
 CC recombinant Bcl-w for therapy, diagnosis, antibody production or  
 CC screening of potential modulators  
 CC  
 XX Sequence 168 AA;  
 SQ  
 Query Match 86.8%; Score 876; DB 2; Length 168;  
 Best Local Similarity 97.0%; Pred. No. 2.2e-87;  
 Matches 163; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MATPASTPTRALVADPVGYKLRQGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60  
 DB 1 MTPASTPTRALVADPVGYKLRQGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60  
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKMEPLVG 120  
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKMEPLVG 120  
 QY 121 QVQDMNVAVLETRLADWTHSSGMAEFTALYGDGALBEARRLRREGNMA 168  
 DB 121 QVQDMNVAVLETRLADWTHSSGMAEFTALYGDGALBEARRLRREGNMA 168  
 Db 121 QVQDMNVAVLETRLADWTHSSGMAEFTALYGDGALBEARRLRREGNMA 168

## RESULT 14

AAO18223 standard; protein; 190 AA.

XX AAO18223;  
 XX  
 XX AAO18223;  
 XX  
 XX 18-SEP-2002 (first entry)  
 XX  
 XX Human Bcl-Rambo BHNO domain related protein #4.  
 DE  
 XX Human; apoptotic signal transduction protein; Bcl-Rambo; BHNO domain;  
 KW

KW cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;  
 KW neurotropic; neuroprotective; antiparkinsonian; virucide; anti-inflammatory;  
 KW immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;  
 KW Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;  
 KW graft versus host disease; autoimmune disease.  
 XX Unidentified.  
 OS  
 XX WO200248353-A2.  
 XX  
 XX 20-JUN-2002.  
 XX  
 XX 12-DEC-2001; 2001WO-EP014597.  
 XX  
 XX 12-DEC-2000; 2000DE-01061766.  
 XX  
 XX 04-JAN-2001; 2001DE-01000280.  
 XX  
 XX (APOT-) APOTECH RES & DEV LTD.  
 XX  
 XX Techopp J, Hofmann K;  
 PI  
 XX WPI; 2002-537627/57.  
 DR  
 XX New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and  
 PT for identifying therapeutic modulators of Bcl-Rambo function.  
 PT  
 XX Disclosure; Fig 1; 61pp; German.  
 XX  
 XX The present invention provides the protein and coding sequences of the  
 CC human Bcl-Rambo apoptotic transcription factor, particularly the BHNO  
 CC domain. The sequences are useful in the treatment of diseases caused by  
 CC incorrectly regulated intracellular signal transduction, including  
 CC cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's  
 CC disease), muscular dystrophy, viral infections (including human  
 CC immunodeficiency virus), autoimmune disease, septic shock, graft versus  
 CC host disease and acute hepatitis. The present sequence is a protein  
 CC described in the exemplification of the invention  
 CC  
 XX Sequence 190 AA;  
 SQ  
 Query Match 80.7%; Score 814.5; DB 5; Length 190;  
 Best Local Similarity 87.0%; Pred. No. 1.4e-80;  
 Matches 168; Conservative 1; Mismatches 21; Indels 3; Gaps 3;  
 QY 1 MATPASTPTRALVADPVGYKLRQGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60  
 DB 1 MATPASAXTXAXVAD-XGYKLRQGYVNGAGPGGPAAD-XHQXRAAGDEFETRFRRT 58  
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKMEPLVG 120  
 DB 59 FSDLAAGLHVTPGSAQQRFTQVSDLEFQGXPNWGXAXAFVFGAALCAESVNKMEPLVG 118  
 QY 121 QVQDMNVAVLETRLADWTHSSGMAEFTALYGDGALBEARRLRREGNMA5VRVTLGVAAL 180  
 DB 119 QXQEXMVAVLYLETXLAX-1HSSGMAEFTALYGDGALBEARRLRREGNMA5VRVTLGVAAL 177  
 QY 161 GALVTVGAFPAFK 193  
 DB 178 GALVTVGAFPAFK 190

## RESULT 15

AAW59884 standard; protein; 365 AA.

XX AAW59884;  
 XX  
 XX AAW59884;  
 XX  
 XX 20-NOV-1998 (first entry)  
 XX  
 XX Amino acid sequence of the cDNA clone Bcl-1-like (HAICH29).  
 DE  
 XX Bcl-1-like (HAICH29); chronic inflammatory disease; allergic reaction;  
 KW immunological disorder; autoimmune disease; anti-infectious agent.  
 KW

XX Homo sapiens.  
 OS  
 XX  
 PN W09831800-A2.  
 XX  
 PD 23-JUL-1998.  
 XX  
 PF 21-JAN-1998; 98WO-US000960.  
 XX  
 PR 21-JAN-1997; 97US-0034204P.  
 PR 21-JAN-1997; 97US-0034205P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (AUCK-) AUCKLAND UNISERVICES LTD.  
 FI Ni J, Rosen CA, Gentz RL, Feng P, Krissansen GW, Su JY;  
 XX  
 XX WPI; 1998-414099/35.  
 DR N-PSDB; AAV41925.  
 XX  
 XX New isolated polynucleotides and encoded polypeptides - used to develop  
 PT products for treating e.g. inflammatory diseases, infections,  
 PT immunological disorders, autoimmune diseases, allergies or tumours.  
 XX  
 PS Claim 1; Fig 12A-12D; 120pp; English.  
 CC This is the amino acid sequence of the cDNA clone Bcl-1-like (HAICH29),  
 CC used in the method of the invention. The products of the clone can be  
 CC used for treating conditions associated with abnormal expression of the  
 CC polypeptides. They can be used for e.g. treating chronic inflammatory  
 CC diseases, immunological disorders, autoimmune diseases, inflammatory  
 CC diseases, various allergies, and as anti-infectious agents. The products  
 CC can also be used for detection and diagnosis  
 XX  
 SQ Sequence 365 AA;

Query Match 75.2%; Score 759; DB 2; Length 365;  
 Best Local Similarity 98.6%; Pred. No. 3.9e-74;  
 Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFYGYKLRQKGYVCGAGPGEPADPLHQMRAAGDEFETFRRT 60  
 |||||  
 Db 1 MATPASAPDTRALVADFYGYKLRQKGYVCGAGPGEPADPLHQMRAAGDEFETFRRT 60  
 QY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFGGPNMGRVAFVFGAALCAESVKNKEPIVG 120  
 |||||  
 Db 61 FSDLAQLHVTTPGSAQQRFTQVSDELFGGPNMGRVAFVFGAALCAESVKNKEPIVG 120  
 QY 121 QVODMNVAYLETRLADWIHSSGW 144  
 |||||  
 Db 121 QVODMNVAYLETRLADWIHSSGW 144

Search completed: February 26, 2004, 11:13:02  
 Job time : 64 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: February 26, 2004, 11:11:52 ; Search time 23 Seconds

(without alignments)  
433.209 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009  
Sequence: 1 MATPASTPDRALVADFGVY.....LTGAVALGALVTGAFPRASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfilest.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1005	99.6	193	1	US-08-798-897-3
2	1005	99.6	193	2	US-08-978-523-3
3	1000	99.1	192	1	US-08-798-897-5
4	1000	99.1	192	2	US-08-978-523-5
5	995	98.6	193	1	US-08-798-897-4
6	995	98.6	193	2	US-08-978-523-4
7	990	98.1	192	1	US-08-798-897-6
8	990	98.1	192	2	US-08-978-523-6
9	759	75.2	365	4	US-09-148-476-696
10	759	75.2	365	4	US-09-010-147B-24
11	428.5	42.5	233	4	US-09-271-014A-6
12	427.5	42.4	233	1	US-08-333-565-59
13	427.5	42.4	233	1	US-08-081-448-6
14	427.5	42.4	233	1	US-08-607-269-24
15	427.5	42.4	233	1	US-08-471-058-14
16	427.5	42.4	233	1	US-08-661-479-59
17	427.5	42.4	233	2	US-08-470-670A-7
18	427.5	42.4	233	2	US-08-471-057-14
19	427.5	42.4	233	3	US-08-481-739-2
20	427.5	42.4	233	3	US-09-167-921-2
21	427.5	42.4	233	3	US-09-323-743-2
22	427.5	42.4	233	4	US-08-461-511A-7
23	427.5	42.4	233	4	US-08-470-865-14
24	427.5	42.4	233	5	PCT-US94-07089-7
25	427.5	42.4	233	5	PCT-US95-04600-24
26	425	42.1	225	3	US-09-101-519-1
27	423.5	42.0	233	1	US-08-607-269-23

28	423.5	42.0	233	5	PCT-US95-04600-23	Sequence 23, Appl
29	412	40.8	236	1	US-08-607-269-22	Sequence 22, Appl
30	412	40.8	236	5	US-09-127-048-9	Sequence 9, Appl
31	412	40.8	236	5	PCT-US95-04600-22	Sequence 22, Appl
32	411.5	40.8	239	1	US-08-112-208C-10	Sequence 10, Appl
33	411.5	40.8	239	1	US-08-248-819A-10	Sequence 10, Appl
34	411.5	40.8	239	2	US-08-337-646A-10	Sequence 10, Appl
35	411.5	40.8	239	2	US-08-856-531-10	Sequence 10, Appl
36	411.5	40.8	239	2	US-08-856-034-10	Sequence 10, Appl
37	411.5	40.8	239	3	US-09-127-048-8	Sequence 8, Appl
38	411.5	40.8	239	3	US-08-927-326-10	Sequence 10, Appl
39	411.5	40.8	239	4	US-09-379-820A-10	Sequence 10, Appl
40	409.5	40.6	239	1	US-08-333-565-51	Sequence 51, Appl
41	409.5	40.6	239	1	US-08-248-819A-12	Sequence 12, Appl
42	409.5	40.6	239	1	US-08-607-269-20	Sequence 20, Appl
43	409.5	40.6	239	1	US-08-471-058-12	Sequence 12, Appl
44	409.5	40.6	239	1	US-08-690-095-4	Sequence 4, Appl
45	409.5	40.6	239	2	US-08-465-485A-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-08-798-897-3  
Sequence 3, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483, 0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-3  
Query Match 99.6%; Score 1005; DB 1; Length 193;  
Best Local Similarity 99.5%; Pred. 5.9e-107;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASTPDRALVADFGVYKLRQGYVCGAPGEPAAADLHQAMRAAGDEFETRRRT 60  
DB 1 MATPASTPDRALVADFGVYKLRQGYVCGAPGEPAAADLHQAMRAAGDEFETRRRT 60  
QY 61 FSDLAQLHTPGSAQGRFTVOVSDELFOGGMGRRLVAFVFGAALCAESVKNEMPELVG 120

Db 61 FSDLAQLHVTGSGAQQRTQVSDELFOGSPNMGRLVAFVFGALCAESVKNKEPVLVG 120  
QY 121 QVQDMWVAVLETRLDWIHSSGMAEFYALYGDGALBEARRLREGNMAVRYTLTGAVAL 180  
Db 121 QVQDMWVAVLETRLDWIHSSGMAEFYALYGDGALBEARRLREGNMAVRYTLTGAVAL 180  
QY 181 GALVTGAFPAK 193  
Db 181 GALVTGAFPAK 193

RESULT 2  
US-08-978-523-3  
; Sequence 3, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Gaestella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ramond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-978-523-3

Query Match 99.6%; Score 1005; DB 2; Length 193;  
Best Local Similarity 99.5%; Pred. No. 5.9e-107;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADVFVGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEPFRFRRT 60  
Db 1 MATPASTPTRALVADVFVGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEPFRFRRT 60  
QY 61 FSDLAQLHVTGSGAQQRTQVSDELFOGSPNMGRLVAFVFGALCAESVKNKEPVLVG 120  
Db 61 FSDLAQLHVTGSGAQQRTQVSDELFOGSPNMGRLVAFVFGALCAESVKNKEPVLVG 120  
QY 121 QVQDMWVAVLETRLDWIHSSGMAEFYALYGDGALBEARRLREGNMAVRYTLTGAVAL 180  
Db 121 QVQDMWVAVLETRLDWIHSSGMAEFYALYGDGALBEARRLREGNMAVRYTLTGAVAL 180

QY 181 GALVTGAFPAK 193  
Db 181 GALVTGAFPAK 193

RESULT 3  
US-08-798-897-5  
; Sequence 5, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Gaestella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ramond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-5

Query Match 99.1%; Score 1000; DB 1; Length 192;  
Best Local Similarity 99.5%; Pred. No. 2.2e-106;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPTRALVADVFVGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEPFRFRRT 61  
Db 1 ATPASTPTRALVADVFVGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEPFRFRRT 60  
QY 62 SDLAQLHVTGSGAQQRTQVSDELFOGSPNMGRLVAFVFGALCAESVKNKEPVLVG 121  
Db 61 SDLAQLHVTGSGAQQRTQVSDELFOGSPNMGRLVAFVFGALCAESVKNKEPVLVG 120  
QY 122 VQDMWVAVLETRLDWIHSSGMAEFYALYGDGALBEARRLREGNMAVRYTLTGAVAL 181  
Db 121 VQDMWVAVLETRLDWIHSSGMAEFYALYGDGALBEARRLREGNMAVRYTLTGAVAL 180  
QY 182 ALVTGAFPAK 193  
Db 181 ALVTGAFPAK 193

RESULT 4  
US-08-978-523-5  
; Sequence 5, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Gaestella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-523-5

Query Match 99.1%; Score 1000; DB 2; Length 192;  
Best Local Similarity 99.5%; Pred. No. 2.2e-106;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ATPASTPDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFFTRFRRTF 61  
DB 1 ATPASTPDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFFTRFRRTF 60  
QY 62 SDLAQLHVTTPGSAQORFTQVSDLPFGGPNWGRVAFVFGALCAESVKNKMEPLVQ 121  
DB 61 SDLAQLHVTTPGSAQORFTQVSDLPFGGPNWGRVAFVFGALCAESVKNKMEPLVQ 120  
QY 122 VQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRTVLTGAVALG 181  
DB 121 VQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRTVLTGAVALG 180  
QY 182 ALVTVGAFPPASK 193  
DB 181 ALVTVGAFPPASK 192

RESULT 5  
US-08-798-897-4  
Sequence 4, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
MEDIUM TYPE: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington

STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-4

Query Match 98.6%; Score 995; DB 1; Length 193;  
Best Local Similarity 98.4%; Pred. No. 8.3e-106;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASPTDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFFTRFRRT 60  
DB 1 MATPASPTDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFFTRFRRT 60  
QY 61 FSDLAQLHVTTPGSAQORFTQVSDLPFGGPNWGRVAFVFGALCAESVKNKMEPLVQ 120  
DB 61 FSDLAQLHVTTPGSAQORFTQVSDLPFGGPNWGRVAFVFGALCAESVKNKMEPLVQ 120  
QY 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRTVLTGAVALG 180  
DB 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRTVLTGAVALG 180  
QY 181 GALVTVGAFPPASK 193  
DB 181 GALVTVGAFPPASK 192

RESULT 6  
US-08-978-523-4  
Sequence 4, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
MEDIUM TYPE: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Emond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-523-4

Query Match 98.6%; Score 995; DB 2; Length 193;  
Best Local Similarity 98.4%; Pred. No. 8.3e-106;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRRT 60  
DB 1 MATPASAPDTRALVEDPVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRRT 60

QY 61 FSDLAQLHVTTPGSAQORFTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120  
DB 61 FSDLAQLHVTTPGSAQORFTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120

QY 121 QVDMWVAVLETRLADWIMHSSGMAEFTLYGDGALAEARRLRBNWMAVRYTLTGAVAL 180  
DB 121 QVDMWVAVLETRLADWIMHSSGMAEFTLYGDGALAEARRLRBNWMAVRYTLTGAVAL 180

QY 181 GALVTYGAFFASK 193  
DB 181 GALVTYGAFFASK 193

RESULT 7  
US-08-798-897-6  
Sequence 6, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Emond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-6

Query Match 98.1%; Score 990; DB 1; Length 192;  
Best Local Similarity 98.4%; Pred. No. 3.1e-105;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTPTRALVADPVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRRT 61  
DB 1 ATPASAPDTRALVEDPVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRRT 60

QY 62 SDLAQLHVTTPGSAQORFTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 121  
DB 61 SDLAQLHVTTPGSAQORFTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120

QY 122 QVDMWVAVLETRLADWIMHSSGMAEFTLYGDGALAEARRLRBNWMAVRYTLTGAVAL 181  
DB 121 QVDMWVAVLETRLADWIMHSSGMAEFTLYGDGALAEARRLRBNWMAVRYTLTGAVAL 180

QY 182 ALVTYGAFFASK 193  
DB 181 ALVTYGAFFASK 192

RESULT 8  
US-08-978-523-6  
Sequence 6, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Emond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear



MOLECULE TYPE: protein  
US-08-978-523-6

Query Match 98.1%; Score 990; DB 2; Length 192;  
Best Local Similarity 98.4%; Pred. No. 3,1e-105;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPSTEDTALVADPFVGYKLRQKGYCGAGPGGAPADPHQMRRAAGDEFFRFRPTF 61  
DB 1 ATPASADPTRALVADPFVGYKLRQKGYCGAGPGGAPADPHQMRRAAGDEFFRFRPTF 60

QY 62 SDLAQLAHVTGSGAQORFTQVSDLFQCGPMNGRLVAFVFGALCAESVKNEMPLVQ 121  
DB 61 SDLAQLAHVTGSGAQORFTQVSDLFQCGPMNGRLVAFVFGALCAESVKNEMPLVQ 120

QY 122 VQDMVAVYLETRLADWTHSSGMAEFTALYDGALEEARLRREGNMAVSRTLTGAVALG 181  
DB 121 VQDMVAVYLETRLADWTHSSGMAEFTALYDGALEEARLRREGNMAVSRTLTGAVALG 180

QY 182 ALVTVGAFPSAK 193  
DB 181 ALVTVGAFPSAK 192

RESULT 9  
US-09-149-476-696  
Sequence 696; Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149, 476  
EARLIER FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040, 162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038, 621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047, 600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 584

EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043, 580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048, 974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056, 886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 879  
EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 75.2% Score 759; DB 4; Length 365;  
Best Local Similarity 98.6%; Pred. No. 2,1e-78;  
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQGYVCGAPGEPADPLHQAAMRAAGDEFTFRRT 60  
DB 1 MATPASAPDRALVADFGYKLRQGYVCGAPGEPADPLHQAAMRAAGDEFTFRRT 60  
QY 61 FSDLAQLHTVPGSAQCRFTQVSDLPFGGNGRVLVFFVFGALCAESYKMEPLVG 120  
DB 61 FSDLAQLHTVPGSAQCRFTQVSDLPFGGNGRVLVFFVFGALCAESYKMEPLVG 120  
QY 121 QVQDMVAVYLETRLADWTHSSGW 144  
DB 121 QVQDMVAVYLETRLADWTHSSGW 144

## RESULT 10

US-09-010-147B-24  
Sequence 24, Application US/09010147B  
Patent No. 6653445  
GENERAL INFORMATION:  
APPLICANT: NI et al.  
TITLE OF INVENTION: Human Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC  
compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-NO. 6653445-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-010-147B-24  
Query Match 75.2% Score 759; DB 4; Length 365;  
Best Local Similarity 98.6%; Pred. No. 2,1e-78;

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Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY 1 MATPASTPTDTALVADFVGYKLRQKGYICGAGPGEGRPADLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFVGYKLRQKGYCGAGPGGPADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHTVMPGSAQOQFTQVSDLEFQGGPNMGLVAFVFGAALCAESVNKEMEPVIG 120
Db 61 FSDLAALQHTVMPGSAQOQFTQVSDLEFQGGPNMGLVAFVFGAALCAESVNKEMEPVIG 120
QY 121 QVQDMNVAVLETRLADWIHSSGGW 144
Db 121 QVQDMNVAVLETRLADWIHSSGGW 144

RESULT 11
US-09-271-014A-6
; Sequence 6, Application US/09271014A
; Patent No. 6395510
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, CRAIG B.
; APPLICANT: BOISE, LAWRENCE H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD-316
; CURRENT APPLICATION NUMBER: US/09/271,014A
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Human
US-09-271-014A-6

Query Match 42.5%; Score 428.5; DB 4; Length 233;
Best Local Similarity 41.1%; Pred. No. 7,3e-41;
Matches 92; Conservative 23; Mismatches 58; Indels 51; Gaps 4

QY 11 RALVADFVGYKLRQKGYVC-----GAGP-----GEGPAA 39
Db 6 RELVVDPLSTYLSQKGYMSQPSVDENRTEAPECTGSEMETPSALINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALQHTVMPGSAQOQFTQ 81
Db 66 NGATAHSSSLDAREVITPMAAVKQALREAGDEFELRYRAFSDLTSLQHTGTAYQSFQ 125
QY 82 VSDLEFQGGPNMGRVAFVFGAALCAESVNKEMEPVIGQVQDMNVAVLETRLADWIHSS 141
Db 126 VVNEIFRDGVNMGRVAFVFGAALCAESVDEKQVLSRLDAMATYTLNDHLEPWIDEN 185
QY 142 GGNAAFTALYGDGALLEARLRLE--GNNAASVRYTLTGAVALGAL 183
Db 186 GGMOTFVELYGNNAAESRKQGERNNRPFLLGMVAGVLLGSL 229

RESULT 12
US-08-333-565-59
; Sequence 59, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

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/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/   APPLICATION NUMBER: US/08/333,565  
/   FILING DATE: 31-OCT--1994  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Smith, William M.  
/ REGISTRATION NUMBER: 30,223  
/ REFERENCE/DOCKET NUMBER: 15726A-000700  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 326-2400  
/ TELEFAX: (415) 326-2422  
/ INFORMATION FOR SEQ ID NO: 59:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 233 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: peptide  
US-08-333-565-59
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Query Match                42.4%; Score 427.5; DB 1; Length 233;  
Best Local Similarity     41.3%; Pred. No. 9.6e+41;  
Matches      93; Conservative    22; Mismatches    57; Indels     53; Gaps     4

OY          11 RALVADPVGYKLRQKY-----Y 28  
| | | | | : | : |  
DB          6 RELAVDFLYSKLQSGYSWQSFDVEENRTAPEGTESEMETPSAINGNPWHLDSPAY 65  
| | | | | : | : |  
OY          29 CGAGRGESPAD-----PLHMAMRAAGEFEETRPRTSSDLDAQHVRPGSAQRFT 80  
| | | | | : | | | | | : | : | : | : | : |  
DB          66 NGA-TGHSSSLDAREVIIPMAVKQLRPADEFLRYRRAPSDLTSQLHTPTGVQSFPE 124  
| | | | | : | : | | | : | : | : | : | : |  
OY          81 QVSSELFCGGNMGRLVAFFVGAAACAESYNKEMEPIVCGOVOMNVYYLETRLADWIHS 140  
|| ||| : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB          125 QVANELPFDDGVNMGRITVAFFSFGALCVESVDKENQVLIVSIAMMATYLNDHLEPWIQE 184  
| | | | | : | : | | | : | : | : | : | : |  
  
OY          141 SGMNAEPFATLYGDGLAEARLRRE-GNWASVRTVLTCGAVAVALGAL 183  
| | | | | : | : | | | : | : | : | : | : |  
DB          185 NGMDTFVELYGNMNAAESRKQGDRPNRWFLTGMTVAGVVLLGSIL 229  
| | | | | : | : | | | : | : | : | : | : |  
  
RESULT 13  
US-08-081-448-6  
Sequence 6, Application US/08081448  
Patent No. 5646008  
GENERAL INFORMATION:  
Applicant: Thompson, Craig B.  
Applciant: Boise, Lawrence H.  
Title Of Invention: Vertebrate Apoptosis Gene:  
TITLE OF INVENTION: Compositions and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSSEE: Arnold, White & Durkee  
STREET: 321 No. 5646008th Clark Street, Suite 800  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/081,448  
FILING DATE: 19930622  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: E. Thomas  
REGISTRATION NUMBER: 33,268

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REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-081-448-6

Query Match          42.4%; Score 427.5; DB 1; Length 233;
Best Local Similarity 40.6%; Pred No. 9.6e-41;
Matches    91; Conservative   23; Mismatches   59; Indels   51; Gaps    4

QY      11 PALVADPVGYKILRKQY-----VCGAGP---GEGPA 39
        |||::|||::|||::|||::|||::|||::|||::|||
DB       6 RELVDPLSYKLSCQGYGSWSPDVEENRTAEPECTESEMTPSAINGNPSMHLADSPAV 65
        :||::|||::|||::|||::|||::|||::|||::|||
QY      40 D-----PLHQANRAGDETFETFRFRFSDLAQLHTPSSAQORFTQ 81
        :||::|||::|||::|||::|||::|||::|||::|||
DB      66 NGATAHSSSLDAREVIYPMAAVAKQALREAGDEFELRYRAFSLSLTQLHPTGTAYQSFEQ 125
        :||::|||::|||::|||::|||::|||::|||::|||
QY      82 VSDLEFGQGPMMGRIVAFVFPGALCAESVNKEMEPLVCQGVDMVAAYLETGLADIHS 141
        |||::|||::|||::|||::|||::|||::|||::|||
DB     126 VNNEIFRGVNGRIYIAFFSGALCVESVDKEMOVLVSRIAAMATYINDLHPWIOEN 185
        |||::|||::|||::|||::|||::|||::|||::|||
QY     142 GWMAEFTALYGDALEEARLRLE--GNMASVTYTLTGAVVALGAL 183
        |||::|||::|||::|||::|||::|||::|||::|||
DB     186 GSWDTFVELYGNNAAESKRKGERRNRMFLTGMTVAGVLLGSL 229
        |||::|||::|||::|||::|||::|||::|||::|||

RESULT 14
US-08-607-269-24
Sequence 24, Application US/08607269
Patent No. 5702897
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607, 269
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226, 876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid

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; TOPOLGY: linear
US-08-607-269-24

Query Match 42.4%; Score 427.5; DB 1; Length 233;
Best Local Similarity 40.6%; Pred. No. 9,6e-41;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKLRQKQY-----VCGAGP-----GEGPAA 39
DB 6 RELVYDFLSIKLQKGYSMSPQSDVEENTTEAPEGESMETPSPAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETRETRRTSDLAALQHLVTPSSAQOQFTQ 81
DB 66 NGATAHSSSDAREVIPAAMVKAQALREADDEFELRYRRAFSDLTSLQHLITPGTAYQSPFQ 125
QY 82 VSDELFGCGNNKRLVAFVFGAALCAESVKNEMEPVQGVQDMMVAYLEFLAMHSS 141
DB 126 VLVLELFPDGNWGRIVAFPSFGALCVESVDKEMQVLRIAMAMATYLNHLEPQEN 185
QY 142 GCMAEFTALYGDGALBEARLRLE--GNMVSVRTVLTLGAVALGAL 183
DB 186 GGMDFVELYGNNAABSKRGQERFRKRWFLTGHTVAGVLLSL 229

RESULT 15
US-08-471-058-14
; Sequence 14, Application US/08471058
; Patent No. 577043
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Leinhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-058-14

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Best Local Similarity 41.3%; Pred. No. 9.6e-41;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

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Qy 11 RALVADFGYKLRQKY-----V 28
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Db 6 RELVVDPLSYKLSQGYGWSQFSDVEENRTEAPGTESEMETPSAINGNPSMHLADSPAV 65
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Qy 29 CGAGPGEGPAD-----PLHQMRAAGDEFEFRFRRTFSDLAOLHTPGSAQQRFT 80
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Db 66 NGA-TGHSSLDAREVTPMAAVKQALREAGDEFELETRRAFSDLTSQHLTPGTAYQSFE 124
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Qy 81 QVSDLEFGGPNMGRVAFVFFGALCAESVKNEMEPVGVQVODMVAYLETRLADWHS 140
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Db 125 QVNNELFRDGVNWRIVAFSFGALCVESVDKEMQVLSRIAAMATYLNHDLEPWIGE 184
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Qy 141 SGWAEFTALYGDGALAEARLRE--GNWASRTVLTGAVALGAI 183
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Db 185 NGGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVVLGSL 229
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Search completed: February 26, 2004, 11:15:37  
Job time : 26 secs

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QY 181 GALVTVGAFASK 193  
Db 181 GALVTVGAFASK 193

## RESULT 2

US-09-925-674A-7  
; Sequence 7, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-925-674A-7

## Query Match

Best Local Similarity 99.1%; Score 1000; DB 9; Length 193;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADPFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGPGSAQORFTQVSDELFOGGRNMGRLVAFVFGALCAESVNKMEPLVG 120  
Db 61 FSDLAQLHVTGPGSAQORFTQVSDELFOGGRNMGRLVAFVFGALCAESVNKMEPLVG 120  
QY 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180  
Db 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180  
QY 181 GALVTVGAFASK 193  
Db 181 GALVTVGAFASK 193

## RESULT 3

US-09-809-391-696  
; Sequence 696, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-391-696

Query Match 75.2%; Score 759; DB 10; Length 365;  
Best Local Similarity 98.6%; Pred. No. 5,7e-74;  
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADPFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60

QY 61 FSDLAQLHVTGPGSAQORFTQVSDELFOGGRNMGRLVAFVFGALCAESVNKMEPLVG 120  
Db 61 FSDLAQLHVTGPGSAQORFTQVSDELFOGGRNMGRLVAFVFGALCAESVNKMEPLVG 120

QY 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180  
Db 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180

## RESULT 4

US-09-882-171-696  
; Sequence 696, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
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; PRIOR APPLICATION NUMBER: 60/040,333  
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; PRIOR FILING DATE: 1997-05-23  
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Query Match 75.2%; Score 759; DB 10; Length 365;  
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[illegible]

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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/101, 482
? FILING DATE: 18-Mar-2002
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/320,157
? FILING DATE: 07-OCT-1994
?
? ATTORNEY/AGENT INFORMATION:
?
? NAME: LEHNHARDT, SUSAN K.
? REGISTRATION NUMBER: 33,943
? REFERENCE/DOCKET NUMBER: 23647-20007.20
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (415) 813-5600
?
? TELEFAX: (415) 494-0792
?
? TELEX: 706141
?
? INFORMATION FOR SEQ ID NO: 14:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 233 amino acids
?
? TYPE: amino acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
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? SEQUENCE DESCRIPTION: SEQ ID NO: 14:
?
? US-10-101-482-14

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Query Match 42.4%; Score 427.5; DB 14; Length 233;
Best Local Similarity 41.3%; Pred. No. 3,6e-38;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4

QY      11 PALVADFVGYKLRQKGY-----Y 28
Db      6 RELVVDLSTYKLSQKGYSSQFSDVEENRTREPGTGESEMETPSAINGNPSWHLADSPAV 65

QY      29 CGAGPGGGSPAD-----PLHOMRPAAGDEFTFRPRRTSDLAALQHTVPGSAQORFT 80
Db      66 NGA-TGHSSTSDAREVTPMAAVKQALNEAGDEFEIRTPRARSDLTSQHTTPGTIVQSE 124

QY      81 QVSDDELQGGGNMGRLVAFVFGAALCAESVNMKEMLPVGVODMVMVAYLETRLADWTHS 140
Db      125 QVNVNELRDRGVGNMGRIVAFEFPGALCVESVDKEMQVLVSHIAAMATYINDHLEPWIQ 184

QY      141 SGGMAEFTALYGGALBEARLRLE--GNWASVRVYLTCVAVLALGAL 183
Db      185 NGGWDTEVELYGNNAAESRRKQDERFNRWFLTGMTVAGVLLGSL 229

RESULT 13
US-10-072-830-4
; Sequence 4, Application US/10072830
; Publication No. US20030103945A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, DONG FENG
; APPLICANT: HUANG, XIZHONG
; APPLICANT: CHEN, GUANG
; APPLICANT: MANUJI, HUSSEINI K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON
; FILE REFERENCE: ERM-105.01
; CURRENT APPLICATION NUMBER: US/10/072.830
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,832
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/272,617
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/289,990
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-072-830-4

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	Query Match	42.4%	Score 427.5	DB 18	Length 233
	Best Local Similarity	40.6%	Pred. No. 3,6e-38		
	Matches	91	Conservative	23	Mismatches 59; Indels 51; Gaps 4
Qy	11	RALVADPVYKLRQKY-----VCGAGP---GEPPA	39		
Db	6	RELVDVDFSYLKSQKXGWSQFSDVEENRTTEAPEEGESEMETPSAINGPSMHLADSIPAV	65		
Qy	40	D-----PLHQARRAGDEPETFRFRFSPLAQQLHTVPSSAOORFPQ	81		
Db	66	NGATRAHSSLARREYTPMAAAVKQALREAGDEBELRYRPAFSULTQMLTTEPTAYQSFEQ	125		
Qy	82	VSDLFQGGPNWGRIVAFVFPGAALCAESVNKEMPELVGVQVDMMVAYLETRLDWIHS	141		
Db	126	VNNELFRGVNMGRIIVAFFSFGCALCVSEVDKEMOVLSRIANMATYLTNDHLEPIQEN	185		
Qy	142	GMAEFRTLGDGALEEABRLRE--GNNAASVTTLTGVALGAL	183		
Db	186	GMDFTFVELYGNNAAAESRKGOERNRNRFLLGTMTAVGVLLDGL	229		

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RESULT 14
US-10-169-223-10
; Sequence 10, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: TSUJIMOTO, Shigeomi
; APPLICANT: TSUJIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537P
; CURRENT APPLICATION NUMBER: US/10/169, 223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 233
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-169-223-10

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Query Match	42.4%	Score 427.5	DB 14	Length 233
Best Local Similarity	40.6%	Pred. NO. 3.6e-38		
Matches	91	Conservative 23	Mismatches 59	Indels 51
			Gaps 4	
Qy	11	RAIVADFWGYKLRQKQY	-----VCGACP-----	-GEGPAA 39
Db	6	RELIVDFLSTYKLSQKGSWQSFSDVEBNRTAEPCESEMETPPASINGNPWHLDSPAY		65
Qy	40	D-----PLHQNRANAGDEPERFRFRFSPLAOLHTPSSAOORFQ		81
Db	66	NGATAHSSLDAREVIEPMAAVAKQALREAGDEBELTIRRFSSLTQOLHTPGTAIOSEFQ		125
Qy	82	VSDBLEFOGQPNWGRVVAFFVFGAALCAESVNMKEPLYGOQVDMMWVAYLETRLADIHSS		141
Db	126	VYNELFRDQVNMGRIVAFPSFCGALCVESVDKEMQVLVRIAMATYILNDHLEPIQEN		185
Qy	142	CGMAEFTLLYDGDALGEARLRLE--GNMAVTVTLTGAVALLCAL		183
Db	186	GGWIDFVELYGNNAAAESRKQGERPNRMLTGMTAGVLLDLSL		229

RESULT 15  
US-10-302-262-2  
Sequence 2, Application US/10302262  
Publication No. US20030191300A1  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Morita, Brett P.

```

1  APPLICANT: Nickoloff, Brian J.
2  APPLICANT: Zhang, QINGQING
3  TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
4  FILE REFERENCE: ISPH-0528
5  CURRENT APPLICATION NUMBER: US/10/302,262
6  PRIOR FILING DATE: 2002-11-21
7  PRIOR APPLICATION NUMBER: US/09/734,846
8  PRIOR FILING DATE: 2000-12-12
9  PRIOR APPLICATION NUMBER: 09/277,020
10 PRIOR FILING DATE: 1998-03-26
11 PRIOR APPLICATION NUMBER: 09/167,921
12 PRIOR FILING DATE: 1998-10-07
13 PRIOR APPLICATION NUMBER: 09/323,743
14 PRIOR FILING DATE: 1999-06-02
15 NUMBER OF SEQ ID NOS: 74
16 SOFTWARE: PatentIn Ver. 2.0
17 SEQ ID NO 2
18 LENGTH: 233
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-10-302-262-2

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Query Match 42.4%; Score 427.5; DB 14; Length 233;  
Best Local Similarity 40.6%; Pred. No. 3.6e-38;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps .4;

CY 11 PALVADPVGVKYLKRGY-----VCGAGP---GEGPPA 39  
          |   |   |   |   |  
Db      6 RELVVDPEFLSYKLDSOKGSWSQFSDVEENRTAPECTGESEMETPSAINGNPMHLADSPAV 65  
  
CY                                --PLHQMRAAGDEFEFRFRPTFSFDLLAAQLHTVPBGAQQOOREPT 81  
          |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  
Db      66 NGATAHSSSLDAREVITPMAAYKQALREAGDBDFELRYRPAFSDULNSQLHITTCITAYQSIEQ 125  
  
CY          82 VSDLEIFQGCPNGRLVAFVFVGALCAESYNKEKEPILVGOVQWMMVAYLETRLADWIHS 141  
          |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  
Db      126 VNNEIFRDGVWGRIIVAFPFSGALCVESYDKEMQVLVSRIAAMMATIYNIDHLEFIQEN 185  
  
CY          142 GGMAEFTLALYGDDGLAEARRLR--GMVASRTVLTGAVALLGAL 183  
          |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  
Db      186 GGWDTFVELLYGNNAASRKQSEPNRFELTGMTVAGVVLLGSL 229

Search completed: February 26, 2004, 11:16:23  
Job time : 36 secs

Job time : 36 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 11:11:02 ; Search time 21 Seconds  
(without alignments)  
884.046 Million cell updates/sec

Title: US-09-508-745-4  
Perfect score: 1009  
Sequence: 1 MATPASTPDRALVADFGV.....LTGNVALGALVTGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	428.5	42.5	233	2	bcl-x long - mouse
2	427.5	42.4	233	2	apoptosis regulator
3	424.5	42.1	233	2	BCL-X protein - ra
4	423.5	42.0	233	2	transforming prote
5	414	41.0	232	2	transforming prote
6	411.5	40.8	239	1	transforming prote
7	411	40.7	236	2	BCL-2 - rat (fragm
8	406	40.2	236	2	transforming prote
9	405	40.1	236	1	transforming prote
10	404.5	40.1	233	2	BCL-X-long - rat
11	402	39.8	236	2	B-cell lymphoma 2
12	378	37.5	190	2	apoptosis regulator
13	377.5	37.4	214	2	apoptosis regulator
14	374.5	37.1	227	2	apoptosis regulator
15	356	35.3	216	2	transforming prote
16	348.5	34.5	199	1	transforming prote
17	345	34.2	205	1	transforming prote
18	277.5	27.5	154	2	transforming prote
19	182	18.0	170	2	gene bcl-2 protein
20	174	17.2	176	2	gene bcl-2 protein
21	171	16.9	211	2	gene bcl-2 protein
22	168	16.7	211	2	gene bcl-2 protein
23	158.5	15.7	192	2	gene bcl-2 protein
24	154	15.3	192	2	gene bcl-2 protein
25	151	15.0	261	2	gene bcl-2 protein
26	150.5	14.9	280	2	apoptosis suppress
27	147.5	14.6	179	2	bcl-2-associated p
28	147.5	14.6	179	2	Bax-delta protein
29	147.5	14.6	218	2	bcl-2-associated p

30	142	14.1	177	2	SS4778	NR-13 protein - qu
31	138.5	13.7	143	2	I38921	bcl-2-associated p
32	138	13.7	255	2	JC7657	Mcl-1a protein - z
33	116	11.5	175	2	I39055	Bcl-2 related - hu
34	116	11.5	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	87	8.6	185	2	B83217	hypothetical prote
37	87	8.6	3433	1	GNWVW	genome polypeptide
38	86.5	8.6	301	2	T36534	probable lipase/es
39	86	8.5	270	2	A12598	dihydrodipicolinat
40	86	8.5	279	2	B97381	dihydrodipicolinat
41	84.5	8.4	358	1	AJICOB	glutamate-ammoma
42	83.5	8.3	872	2	G98026	alanine-tRNA ligase
43	83.5	8.3	872	2	H93160	alanyl-tRNA synthet
44	83	8.2	3430	1	GNWVW	genome polypeptide
45	81.5	8.1	886	2	A32758	beta-amyloid-like

## ALIGNMENTS

RESULT 1  
bcl-x long - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence #revision 02-Jul-1996 #text\_change 28-Jul-2003  
C/Accession: I49056; S52866  
R/Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A>Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A/Reference number: I49055; MUID:9505604; PMID:7963517  
A/Accession: I49056  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-233 <RES>  
A/Cross-references: EMBL:U0101; NID:9506647; PID:AAA82173.1; PID:9506648  
R/Kamesaki, H.; Michoud, G.Y.; Takatsu, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A/Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line throu  
A/Reference number: S52866  
A/Accession: S52866  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-233 <XAM>  
A/Cross-references: EMBL:X83574; NID:9695622; PID:CAA58557.1; PID:9695623  
C/Superfamily: bcl apoptosis regulator, inhibitory type  
Query Match 42.5%; Score 428.5; DB 2; Length 233;  
Best Local Similarity 41.3%; Pred. No. 2.2e-32;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;  
QY 11 PALVADFGVGYKLRKQGY-----V 28  
DB 6 RELVVDPLSLKYLQKQGSWSQFSDVEENRTREAPETREAPETSAINGNSPWLADSPAV 65  
QY 29 CGAGPGECPAAD-----PLHQAMPACDEETRETRFRPSDLAQLHTPGSAOQRF 80  
DB 66 NGA-TGHSSSLIDREVI-PMAAVKQALREAGDEFELRYRAFSDLTSLHTTPGAYOSFE 124  
QY 81 QVSDLEFGGPNMGRVAFVPGALCAESVNMMEVLVQGVQVDMWVAVETRLADWTHS 140  
DB 125 QVNELEFRDGVNMGRIAFVPGALCVESVDKEMOVLVSRIASWMTYVINDHLEPIQE 184  
QY 141 SGGMAEFTALYDGALEEARLR--GNWASVTVTLGAVAGAL 183  
DB 185 NGCMDFTFVDLYGNNAAEKRGQERFRWFLTGMTAVAGVLLSL 229  
RESULT 2  
B47537  
apoptosis regulator bcl-xl - human  
N/Alternate names: bcl-2-related protein  
N/Contains: apoptosis regulator bcl-xS

C.Species: Homo sapiens (man)  
C.Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 28-Jul-2003  
C.Accession: B47537; C47537  
R.Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
Cell 74, 597-608, 1993  
A.Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
A.Reference number: A47537; MUID:93364977; PMID:8358789  
A.Accession: B47537  
A.Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-233 <BOI>  
A.Cross-references: GB:L20121; NID:9510900; PIDN:CAA80661.1; PID:9510901  
A.Accession: C47537  
A.Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-69, G', 71-125, 189-233 <BO2>  
A.Cross-references: GB:L0122; NID:9623236; PIDN:CAA80662.1; PID:9623237  
C.Genetics:  
A:Gene: GDB:BCL2L  
A:Cross-references: GDB:228079  
C:Superfamily: bcl apoptosis regulator, inhibitory type  
C:Keywords: alternative splicing; apoptosis  
F:1-233/Product: apoptosis regulator bcl-xl #status predicted <MAT>  
F:1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>  
  
Query Match 42.4%; Score 427.5; DB 2; Length 233;  
Best Local Similarity 40.6%; Pred. No. 2.8e-32;  
Matches 91; Conservative 23; Mismatches 39; Indels 51; Gaps 4;  
  
QY 11 PALVADPFGVYKLRQKQY-----VCGAP---GEGPAA 39  
DB 6 RELVVDPLSTYKLSQKGYSGFSQSDVEENRTEAPECTESEMTPSAINGNPSWHLADSPAV 65  
  
QY 40 D-----PLHQMRAGDEFETFRFTFSDLAQLHTVTPGSAOQRTQ 81  
DB 66 NGATAHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFDLTQSOLHTTPTAYQSPFQ 125  
  
QY 82 VSDLEFQGGPNMGRIVAFVFGALCAESVUNKEMPELVGOVDMVAVYLEFTLADWIMSS 141  
DB 126 VNELFRDGVNMGRIIVAFVFGALCVESVDKEMQVLVSRIAMATYLNHLEPWIDEN 185  
  
QY 142 GMAEFTALYGDALBEARLRLE--GNMASVTVLTGAVLAL 183  
DB 186 GMDTFVLDYGNMAAESRKQGERFRNRFMTGMTVAGVLLGSL 229  
  
RESULT 3  
S51761  
BCL-X protein - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 28-Jul-2003  
C.Accession: S51761; S51762  
R.Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A.Reference number: S51761  
A.Accession: S51761  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-233 <MIC>  
A.Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57886.1; PID:9607177  
A.Experimental source: embryonic; brain  
A.Accession: S51762  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-125,189-233 <MI2>  
A.Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57887.1; PID:9607178  
A.Experimental source: embryonic; brain  
A>Note: smaller form due to splicing  
C.Genetics:  
A:Introns: 125/3  
A:Superfamily: bcl apoptosis regulator, inhibitory type  
Query Match 42.1%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 5.3e-32;  
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;  
  
QY 13 LVADPFGVYKLRQKQY-----VCG 30  
DB 8 LVVFLSTYKLSQKGYSGFSQSDVEENRTEADETEPEREPTSAINGNPSWHLADSPAVNG 67  
  
QY 31 AGPEGAPAD-----PLHQMRAGDEFETFRFTFSDLAQLHTVTPGSAOQRTQV 82  
DB 68 A-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFDLTQSOLHTTPTAYQSPFQV 126  
  
QY 83 SDELFGGPNMGRIVAFVFGALCAESVUNKEMPELVGOVDMVAVYLEFTLADWIMSSG 142  
DB 127 VNELFRDGVNMGRIIVAFVFGALCVESVDKEMQVLVSRIAMATYLNHLEPWIDENG 186  
  
QY 143 GMAEFTALYGDALBEARLRLE--GNMASVTVLTGAVLAL 183  
DB 187 GMDTFVLDYGNMAAESRKQGERFRNRFMTGMTVAGVLLGSL 229  
  
RESULT 4  
A37332  
Transforming protein (bcl-2-alpha) - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 28-Jul-2003  
C.Accession: A37332; S35453  
R.Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie  
A.Reference number: A37332; MUID:92375724; PMID:1508712  
A.Accession: A37332  
A.Status: nucleic acid sequence not shown  
A.Molecule type: DNA  
A.Residues: 1-233 <EGU>  
A:Cross-references: EMBL:D11381  
C.Genetics:  
A:Introns: 189/3  
C:Superfamily: bcl apoptosis regulator, inhibitory type  
C:Keywords: mitochondrion; transforming protein; transmembrane protein  
  
Query Match 42.0%; Score 423.5; DB 2; Length 233;  
Best Local Similarity 38.0%; Pred. No. 6.5e-32;  
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;  
  
QY 9 DTRALVADPFGVYKLRQKGYCGAG-----PGGAPADP----- 41  
DB 10 DNREIVLKYIHYKLSQKGYDWAAGEDRPVPAPAPAPAAVAAGASSHHRRPPGSA 69  
  
QY 42 -----LHQMRAGDEFETFRFTFSDLAQLHTVTPGSAOQRTQVSD 84  
DB 70 AASEVPAEGLRPAAPGVHLLRQAGDEFSSRRYQDFAQMSGQLHTFTAHGRFAVVE 129  
  
QY 85 ELFGGPNMGRIVAFVFGALCAESVUNKEMPELVGOVDMVAVYLEFTLADWIMSSG 144  
DB 130 ELFRDGVNMGRIIVAFVFGALCVESVREMSPLVDNLTATWTEYLNHLEPWIDEN 189  
  
QY 145 AEFTALYGDALBEARLRLEGNMASVTVLTGAVLALVTVGAFFASK 193  
DB 190 DAFVELYGN---SMRPLDFSWISLKITLS-LVVGACITLGAYLGRK 233  
  
RESULT 5  
S24390  
Transforming protein (Bcl-2) homolog - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 28-Jul-2003  
C.Accession: S24390  
R.Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.  
Biochim. Biophys. Acta 1132, 109-113, 1992  
A>Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue  
A.Reference number: S24390; MUID:92379084; PMID:1511008  
A.Accession: S24390  
A.Status: preliminary



A:Molecule type: mRNA  
A:Residues: 1-232 <CAZ>  
A:Cross-references: EMBL:Z11961; NID:g62969; PIDDN:CAA78018.1; PID:g62970  
C:Superfamily: bcl apoptosis regulator, inhibitory type  
C:Keywords: mitochondrion; transmembrane protein

Query Match      41.0% Score 414; DB 2; Length 232;  
Best Local Similarity 37.7%; Pred. No. 4.9e-31;  
Matches    86; Conservative    32; Mismatches    62; Indels    48; Gaps    4;

OY                  9 DTRALVADFGVKLRQKGYCGAG-----PGEGPADP----- 41  
| | : : : : |||| : ||||  
DB         10 DNREILVTKHYHTLSGQGTYMAGEDRPPVPAPAPAARAAVAAGAASHHRPSPARTL 69  
  
OY                  42 -----LHQARRAADGEFETFPRTTSPDLAQHLVTGPSAOORFTVOSEP 85  
| | : : : : |||| : ||||  
DB         70 LTVRCPLRLGCAPPGVHALLROAGDEFRRYYQRPFQAOMSGOLHTPTATGRFAVVARE 129  
  
OY                  86 LRGGNGNRGLVAFPVVGALLCAESVNKEMLPGVCQVDMMWAVYLETRLADMHSISGWNA 145  
| | : : : : |||| : ||||  
DB         130 LPFDGNWNRIIVAFFEFGVNCVESNVREMSPLVDNIAITMTTEYNRHLMNIQDNGMD 189  
  
OY                  146 EFPAFLGDGALBEARRLEGNMASVRFTVLTAVALCALVTCGAFFASK 193  
| | : : : : |||| : ||:  
DB         190 APVELYXGN----SMRPPLDFPSWISTKLTL--LVLVGACITLGAYGHK 232

RESULT 6  
TVHUAI  
transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 28-Jul-2003  
C:Accession: C37332; A29409; S02452; A24428; A27622; B27622  
R:Eguchi, Y.; Swert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A:Reference number: A37332; PMID:92375724; PMID:1508712  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-239 <EGU>  
A>Note: This report is a correction  
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986  
A>Title: Analyses of the structure, transcripts, and protein products of bcl-2, the genes responsible for lymphoma formation in mice and man  
A:Reference number: A29409; PMID:86259760; PMID:3523487  
A:Accession: A29409  
A:Molecule type: RNA  
A:Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>  
A:Cross-references: GB:MI1394; NID:gi179366; PIDDN:AAS1813.1; PID:gi179367  
A>Note: This sequence has been corrected in reference A27332  
R:Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Koremeyer,  
EMBO J. 7, 123-131, 1988  
A>Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene  
A:Reference number: S02452; PMID:88196071; PMID:2834197  
A:Accession: S02452  
A:Molecule type: mRNA  
A:Residues: 1-239 <SPT>  
R:Clery, M.L.; Smith, S.D.; Sklar, J.  
Cell 47, 19-28, 1986  
A>Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer element construct  
A:Reference number: A24428; PMID:87002488; PMID:287599  
A:Accession: A24428  
A:Molecule type: RNA  
A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>  
A:Cross-references: GB:MI14745; NID:gi179370; PIDDN:AAS5591.1; PID:gi179371  
R:Hua, R.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.  
Oncogene Gen. 2, 263-275, 1988  
A>Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: evidence from complementary DNA sequencing studies  
A:Reference number: A27622; PMID:88217344; PMID:3285501  
A:Accession: A27622  
A:Molecule type: mRNA  
A:Residues: 1-58, 'T', 60-239 <HUD>

A:Accession: B27622  
A:Molecule type: DNA  
A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>  
A>Note: The sequence was determined from the germline gene  
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation  
C:Genetics:  
A:Gene: GDB:BCL2  
A:Cross-references: GDB:119031; OMIM:151430  
A:Map position: 18q21.3-18q21.3  
C:Function:  
A:Description: blocks apoptosis in hematopoietic cells  
C:Superfamily: bcl apoptosis regulator, inhibitory type  
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 40.8%; Score 411.5; DB 1; Length 239;  
Best Local Similarity 37.0%; Pred. No. 8.6e-31;  
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

9 DTRALVADPVGYKLRQKGYCGAG-----PGE----- 35  
10 DNRREIMVKTIHYKLSRGYEMDAGDVGARPGAAACGICSSQGHPRHRAASDPVART 69  
36 -----GPAADP-----LHOAMRAAGDEPFRFRRTSSDLAOLHTVPGSAQR 78  
70 SPLQTPAARGAAGPALSPFPVPVHLLTRQAGDDFSRRYRRDPFAEMSSQLHTLFTTARGR 129  
79 FTQVSDLEFQGGPNMGRLLAFAFVFGAALCAESYNKMEPLVGVQODMMVAVLETRLAMI 138  
130 FATVVEELRPDGGNMGRIVAFEFEGGVMCVESYNREMSPLVDNIALMWTETLNRLHTWI 189  
139 HSSGGAFTALYGDALAEARLRREGNMASVTRLVGLAVALGALTVGAFPAK 193  
190 QDNGMDAFLVELYG-----PSMRPLPFPMSWLSKTLTSLAL-VGACITLGAATLGHK 239

RESULT 7  
167432  
BCL-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 28-Jul-2003  
C:Accession: 167432  
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin  
constitutive bcl-2 and bcl-X-long messenger ribonucleic acid levels.  
A:Reference number: 153295; MUID:95129487; PMID:7828536  
A:Accession: 167432  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: EMBL:U34964; NID:G1004378; PIDN:AAA77687.1; PID:G1004379  
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.7%; Score 411; DB 2; Length 236;  
Best Local Similarity 36.2%; Pred. No. 9.6e-31;  
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

9 DTRALVADPVGYKLRQKGY----- 27  
10 DNRREIMVKTIHYKLSRGYEMDAGDDEASPLRRAPTGIFSPESNRPVNRHDTAART 69  
28 -----VCGAGPEGPAADPLHOAMRAAGDEPFRFRRTSSDLAOLHTVPGSAQR 81  
70 SPLRPLVANAGPALSPFPVPVHLLTRRAAGDDFSRRYRRDPFAEMSSQLHTLFTTARGPAT 129  
82 VSDLEFQGGPNMGRLLAFAFVFGAALCAESYNKMEPLVGVQODMMVAVLETRLAMI 141  
130 VVEELRPDGGNMGRIVAFEFEGGVMCVESYNREMSPLVDNIALMWTETLNRLHTWI 189  
142 GGAAFTALYGDALAEARLRREGNMASVTRLVGLAVALGALTVGAFPAK 193  
190 GGMDAFLVELYG-----PSMRPLPFPMSWLSKTLTSLAL-VGACITLGAATLGHK 236

RESULT 8  
 153744 gene bcl-2 protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 28-Jul-2003  
 C:Accession: 153744  
 R:Saco, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
 Gene 140, 291-292, 1994  
 A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
 A:Reference number: 153744; MUID:94193015; PMID:8144041  
 A:Accession: 153744  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <RES>  
 A:Cross-references: GB:LI4680; NID:9408946; PIDN:AAA53662.1; PID:9408947  
 C:Genetics:  
 A:Gene: bcl-2  
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.2%; Score 406; DB 2; Length 236;  
 Best Local Similarity 35.8%; Pred. No. 2.8e-30;  
 Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;  
 9 DTRALVADPVGYKLRQKGY-----PG----- 34  
 10 DNREIVMKYIHKLSQGYEMTGDSDAPLAAAPTCIFSPQPSNTPAVHRTAART 69  
 28 -----VCGAGPEGPAADPLHQMRAGDEFETFRFTSDLAQLHVTGSAQQRFTQ 81  
 70 SPLRPVLANAGPALSPVPVHLTLRRAGDDPSRRYRDFAMSSQLHLTPFTARGPAT 129  
 82 VSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVGVQVDMVAVLETRLADWTHS 141  
 130 VSEELFRGVNMGRIVAFFEFGVNCSVNSKMSPLVDNIALMWTETLNRHLTWIDN 189  
 142 GGMAEFTALYGDGALAEARLRREGNMAVSRTVLTGAVALGALVTGVAFFASK 193  
 190 GGMDFVFLYG----PSMRPLDFPSWLSTKTLISL--VGACITTLGAYLGHK 236  
 Db

RESULT 9  
 transforming protein bcl-2-alpha - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 28-Jul-2003  
 C:Accession: A25960; E37332  
 R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
 Cell 49, 455-463, 1987  
 A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog  
 A:Reference number: A90893; MUID:87187643; PMID:3032455  
 A:Accession: A25960  
 A:Molecule type: DNA  
 A:Residues: 1-236 <NEG>  
 A:Cross-references: GB:LI1532; GB:MI6506; NID:9468336; PIDN:AAA37282.1; PID:9387109  
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety  
 A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: E37332  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: DNA  
 A:Residues: 1-33, 'E', 34-220, 'AL', 223-236 <EGU>  
 C:Genetics:  
 A:Gene: BCL2  
 A:Introns: 192/3  
 C:Superfamily: bcl apoptosis regulator, inhibitory type  
 C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro  
 Query Match 40.1%; Score 405; DB 1; Length 236;  
 Best Local Similarity 37.1%; Pred. No. 3.5e-30;  
 Matches 86; Conservative 33; Mismatches 61; Indels 52; Gaps 5;

QY 9 DTRALVADPVGYKLRQKGYCGAG-----PG----- 34  
 Db 10 DNREIVMKYIHKLSQGYEMDADADAAPLGAAPTCIFSPQPSNMPAVHREMAART 69  
 QY 35 -----EGPAADP---LHQMRAGDEFETFRFTSDLAQLHVTGSAQQRFTQ 81  
 Db 70 SPLRPVLANAGPALSPVPVHLTLRRAGDDPSRRYRDFAMSSQLHLTPFTARGPAT 129  
 QY 82 VSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVGVQVDMVAVLETRLADWTHS 141  
 Db 130 VSEELFRGVNMGRIVAFFEFGVNCSVNSKMSPLVDNIALMWTETLNRHLTWIDN 189  
 QY 142 GGMAEFTALYGDGALAEARLRREGNMAVSRTVLTGAVALGALVTGVAFFASK 193  
 Db 190 GGMDFVFLYG----PSMRPLDFPSWLSTKTLIS--LPWVGACITTLGAYLGHK 236

RESULT 10  
 167431 BCL-X-Long - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 28-Jul-2003  
 C:Accession: 167431  
 R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
 Endocrinology 136, 232-241, 1995  
 A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin  
 constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.  
 A:Reference number: 153295; MUID:95129487; PMID:7828536  
 A:Accession: 167431  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <RES>  
 A:Cross-references: EMBL:U34963; NID:91004376; PIDN:AAA7686.1; PID:91004377  
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.1%; Score 404.5; DB 2; Length 233;  
 Best Local Similarity 39.6%; Pred. No. 3.8e-30;  
 Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;  
 11 RALVADPVGYKLRQKGY-----V 28  
 6 RELVDFLSTYKLSQGYSWQSFDVENRTAPEETPERETPSAINGNPSMHLADSPAV 65  
 29 CGAGPEGPAAD-----PLHQMRAGDEFETFRFTSDLAQLHVTGSAQQRFT 80  
 66 NGA-TGHSSSIDAREVLPMVAVKQALRAAGDEFELRYRARASDLSQHLTPGTVYQSE 124  
 QY 81 QVSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVGVQVDMVAVLETRLADWTHS 140  
 Db 125 QVNVLEFRDGVNMGRIVASSFGALCVESVDKEMQVLSRIASMMATYLDHLEPWIQE 184  
 QY 141 SGMAEFTALYGDGALAEARLRREGNMAVSRTVLTGAVALGAL 183  
 Db 185 NGMDFVFLYGNMTAPESRKQGERFNRFLTGMTVAGVLLGSL 229

RESULT 11  
 JCT383 B-cell lymphoma 2 protein - Chinese hamster  
 C:Species: Cricetus griseus (Chinese hamster)  
 C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 28-Jul-2003  
 C:Accession: JCT383  
 R:Tomicic, M.T.; Christmann, M.; Kalna, B.  
 Biochem. Biophys. Res. Commun. 275, 899-903, 2000  
 A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.  
 A:Reference number: JCT383  
 A:Contents: Ovary  
 A:Accession: JCT383  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <TOM>  
 A:Cross-references: GB:A0271720  
 C:Comment: This protein has anti-apoptotic function, and supports cell survival.  
 C:Genetics:



transforming protein (bcl-2-beta) - chicken

C:Species: Gallus gallus (chicken)

C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 28-Jul-2003

C/Accession: B37332; S35452

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues

A/Reference number: A37332; MUID:92375724; PMID:1508712

A/Accession: B37332

A>Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-216 <EGU>

A/Cross-references: EMBL:D11381; EMBL:D11382

C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 35.3%; Score 356; DB 2; Length 216;

Best Local Similarity 38.4%; Pred.No. 1.1e-25;

Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps 2;

```

QY      9 DTRALVADPVGKLRKRGVVCAG-----PGEPPADP----- 41
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     10 DNRRLVLTHTYKLSGRGTDWAGSDRPVPAPAPAAAPAAVAAAGASSHRRPBPQSA 69
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     42 -----LHQAARAGDEPFRFRRTFSDLAQLHVTGSAQQRFTQVSD 84
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     70 AASEVPAPAGLRPAPPGVHLALRQAGDEFRRYQDFQMSQGLHPTFAHGRFVAIVE 129
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     85 ELFGGPNWGRVAPFVFGAALCAESVNTKEMEPVVGQVQDMMVAILETPLADWHSQGM 144
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     130 ELFRDGVNMGRIVAFEFEGVNCVSVNREMSPLVDNIATWMTYLNRIHNMIDNGMW 189
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     145 AEFTA 149
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     190 VRACA 194

```

Search completed: February 26, 2004, 11:15:02  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:07:17 ; Search time 18 Seconds

(without alignments)  
558.308 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009

Sequence: 1 MATPASTPDRALVADVEGV.....LTGAVLGLATVGAFFASK 193

Scoring table: BLOSUM62

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1009	100.0	193	1	BCLM_MOUSE
2	1000	99.1	193	1	BCLW_HUMAN
3	650.5	64.5	228	1	ARI_XENLA
4	432.5	42.5	229	1	BCLX_CHICK
5	431.5	42.8	233	1	BCLX_PIG
6	428.5	42.5	233	1	BCLX_MOUSE
7	428.5	42.5	233	1	BCLX_RAT
8	427.5	42.4	233	1	BCLX_HUMAN
9	423.5	42.0	233	1	BCLX_CHICK
10	415.5	41.2	229	1	BCL2_BOVIN
11	413	40.9	236	1	BCL2_RAT
12	412	40.8	236	1	BCL2_MOUSE
13	411.5	40.8	239	1	BCL2_HUMAN
14	402	39.8	236	1	BCL2_CRITO
15	369	36.6	204	1	ARI1_XENLA
16	175.5	17.4	208	1	BAK_MOUSE
17	171	16.9	211	1	BAK_HUMAN
18	168	16.7	211	1	BAK2_HUMAN
19	156.5	15.5	192	1	BAXA_MOUSE
20	155.5	15.4	192	1	BAXA_RAT
21	154	15.3	192	1	BAXA_HUMAN
22	151	15.0	280	1	CBX9_HUMAN
23	148	14.7	192	1	BAXA_BOVIN
24	147.5	14.6	218	1	BAXB_HUMAN
25	142	14.1	177	1	NR13_CRITA
26	138.5	13.7	143	1	BAXD_HUMAN
27	137.5	13.6	271	1	CBX9_CABER
28	116	11.5	175	1	BFL1_HUMAN
29	116	11.5	175	1	BFL1_HUMAN
30	115	11.4	194	1	BCLB_HUMAN
31	105	10.4	172	1	BFL1_MOUSE
32	99.5	9.9	179	1	BAR_ASFM2
33	98.5	9.8	179	1	BAR_ASFB7

## ALIGNMENTS

RESULT 1	ID	BCLM_MOUSE	STANDARD:	PRT:	193 AA.
AC	P70345				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Apoptosis regulator Bcl-2 (Bcl-2-like 2 protein).				
GN	BCL2L2 OR BCLM.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96358615; PubMed=6761287;				
RA	Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,				
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;				
RT	"bcl-2, a novel member of the bcl-2 family, promotes cell survival.,"				
RL	Oncogene 13:665-675(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/10J;				
RX	MEDLINE=98160183; PubMed=9500547;				
RA	Rosa A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,				
RA	Russell L.D., Macgregor G.R.;				
RT	"testicular degeneration in Bclw-deficient mice.,"				
RL	Nat. Genet. 18:251-256(1998).				
CC	- FUNCTION: Promotes cell survival.				
CC	- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and				
CC	in a wide range of tissues, with highest levels in brain, colon,				
CC	and salivary gland.				
CC	- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic				
CC	function.				
CC	- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.				
CC	- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.				
CC	- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.				
CC	- SIMILARITY: Belongs to the Bcl-2 family.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> ).				
CC	-----				
DR	EMBL; U59746; AAB09056.1; -				007818 african swi
DR	EMBL; AF030769; AAB86430.1; -				P54924 bradyrhizob
DR	HSSP; Q07817; IMAZ.				P14335 k genome po
DR	MGG; MG1:108052; Bcl212.				Q8uiv8 agrobacteri
DR	InterPro; IPR000309; Bcl2_BH.				P23712 lactuca sat
DR	InterPro; IPR003093; Bcl2_BH4.				Q97q48 streptococc
DR	InterPro; IPR002475; Bcl2_family.				O8dpc7 streptococc
DR	Pfam; PF00452; Bcl-2; 1.				P06535 w genome po
					P14599 drosophila
					O28285 archaeoglob
					P14403 j genome po
					P32866 j genome po

```

DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS00062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS00063; BH4_2; 1.
DR Apoptosis.
KM Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 1009; DB 1; Length 193;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGGAPADPLHQMRAAGDEFETRFRRT 60
DB 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGGAPADPLHQMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHTVTPGSAQOQFTQVSDLPFGGPMWGRLVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHTVTPGSAQOQFTQVSDLPFGGPMWGRLVAFVFGAALCAESVKNKEPVLVG 120
QY 121 QVQDMMVAVLETRLDMDIHSSGGMAFETLXGDSALEERRLREGVMASVRTLGAVAL 180
DB 121 QVQDMMVAVLETRLDMDIHSSGGMAFETLXGDSALEERRLREGVMASVRTLGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 2
BCLM HUMAN STANDARD; PRT; 193 AA.
ID BCLM_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2 (Bcl-2-like 2 protein).
GN BCL2L2 OR BCLW OR KIAA0271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-2, a novel member of the bcl-2 family, promotes cell survival.";
RT Oncogene 13:665-675(1996).
RN [2];
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RC MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0289) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RT DNA Res. 3:321-329(1996).
RN [3];
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedl T.B., Toshiyuki S., Carinini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fajay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U59747; AAB09055.1; -.
CC EMBL: D87461; BAA19666.1; -.
CC EMBL: BC021198; AAH21198.1; -.
CC HSP: 007817; IMAZ.
CC GeneW: HGNC:995; BCL2L2.
CC MIM: 601931; -.
CC GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO: GO:0006916; P:anti-apoptosis; TAS.
CC GO: GO:0007283; P:spermatogenesis; TAS.
CC InterPro: IPR000712; BCL2_BH.
CC InterPro: IPR003093; BCL2_BH4.
CC InterPro: IPR002475; BCL2_family.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC PROSITE: PS00062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS00063; BH4_2; 1.
CC Apoptosis.
KM Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match
Best Local Similarity 99.1%; Score 1000; DB 1; Length 193;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGGAPADPLHQMRAAGDEFETRFRRT 60
DB 1 MATPASTPTRALVADPFGYKLRQKGYCGAGPGGAPADPLHQMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHTVTPGSAQOQFTQVSDLPFGGPMWGRLVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHTVTPGSAQOQFTQVSDLPFGGPMWGRLVAFVFGAALCAESVKNKEPVLVG 120

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Db      61 FSDLAQLHTVPSGAQORFTQVSDLEFGCGNMGRLVAFVFGAALCAESVKNEMEPLVG 120
Qy      121 QVQWMVAAYLETRLDADWTHSSGWAFFETALYGDGALBEARLRGNMAVSTVLTGAVAL 180
Db      121 QVQWMVAAYLETRLDADWTHSSGWAFFETALYGDGALBEARLRGNMAVSTVLTGAVAL 180
Qy      181 GALVTGAFPAASK 193
Db      181 GALVTGAFPAASK 193

RESULT 3
ARI_XENLA
ID      ARI_XENLA      STANDARD;      PRT;      228 AA.
AC      Q91827;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Apoptosis regulator Bcl-2 (Fragment).
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC      Xenopodidae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Head;
RX      MEDLINE=95331613; PubMed=7607538;
RA      Cruz-Reyes J., Tata J.R.;
RT      "Cloning, characterization and expression of two Xenopus bcl-2-like
RT      cell-survival genes.";
RL      Gene 158:171-179(1995).
CC      -1- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC      -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC      -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC      brain of mid-metamorphic to post-metamorphic tadpoles and
CC      adults, where an increase of several fold has been observed.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC      -1- SIMILARITY: Belongs to the Bcl-2 family.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; X82462; CA57845.1; -.
DR      HSSP; Q07817; IM42.
DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; BCL2_family.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.
DR      SMART; SM00265; BH4; 1.
DR      PROSITE; PS01080; BH1; 1.
DR      PROSITE; PS01258; BH2; 1.
DR      PROSITE; PS50062; BCL2_FAMILY; 1.
KM      Apoptosis; Transmembrane.
FT      NON_TER      1
FT      DOMAIN      120 139      BH1.
FT      DOMAIN      171 186      BH2.
FT      TRANSMEM      207 227      POTENTIAL.
SQ      SEQUENCE      228 AA; 25068 MW; C499D449A585F8A9 CRC64;
Query Match      64.5%; Score 650.5; DB 1; Length 228;
Best Local Similarity      68.5%; Pred. No. 4e-51;
Matches      126; Conservative      20; Mismatches      35; Indels      3; Gaps      1;
Qy      10 TRALVADFGVYKLRQKGVGAGGEGRAADPLQAMAAADDEFTTRRTFFSDLAQLH 69

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Db      48 SRALVEDLVRYKLCQGRSLV---PEPSGASCALHSARAGDEFEERFRQAFSEISTQIH 104
Qy      70 VTPGSAQORFTQVSDLEFGCGNMGRLVAFVFGAALCAESVKNEMEPLVQVQVDMVAY 129
Db      105 VTPGSAQORFTQVSDLEFGCGNMGRLVAFVFGAALCAESVKNEMEPLVQVQVDMVAY 164
Qy      130 LETRLADWTHSSGWAFFETALYGDGALBEARLRGNMAVSTVLTGAVALGALVTGAF 189
Db      165 LETRLADWTHSSGWAFFETALYGDGALBEARLRGNMAVSTVLTGAVALGALVTGAL 224

Qy      190 FASK 193
Db      225 FASK 228

RESULT 4
BCLX_CHICK
ID      BCLX_CHICK      STANDARD;      PRT;      229 AA.
AC      Q07815; Q98908;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN      BCL2L OR BCLX OR BCL-X.
OS      Gallus gallus (chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM SHORT).
RX      MEDLINE=93364977; PubMed=8358789;
RA      Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA      Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT      "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT      of apoptotic cell death.";
RL      Cell 74:597-608(1993).
CC      (2)
CC      SEQUENCE FROM N.A. (ISOFORM LONG).
CC      STRAIN=Hubbard White Mountain; TISSUE=Testis;
CC      MEDLINE=97264485; PubMed=910311;
CC      Villagra X., Mezquita C., Mezquita J.;
CC      "Differential expression of bcl-2 and bcl-x during chicken
CC      spermatogenesis.";
CC      Mol. Reprod. Dev. 47:26-29(1997).
CC      -1- FUNCTION: Dominant regulator of apoptotic cell death. The long
CC      form displays cell death repressor activity, whereas the short
CC      isoform promotes apoptosis (By similarity).
CC      -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC      envelope (By similarity).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=Long;
CC      IsoId=Q07816-1; Sequence=Displayed;
CC      Name=Short;
CC      IsoId=Q07816-2; Sequence=VSP_000514;
CC      -1- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC      development.
CC      -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC      function. Interact BH1 and BH2 domains are required for anti-
CC      apoptotic activity (By similarity).
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC      -1- SIMILARITY: Belongs to the Bcl-2 family.
CC      -----
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Oy		141	SCGMFEPTALYDGALEEARRE--GNVASRTVLTGVALGAL	183
Dd		185	NGCHDTFVELYGNMAAAESKRGERRNRFLTGMLTAGVLLGLSL	229

  

RESULT 6					
BCLX_MOUSE	ID	BCLX_MOUSE	STANDARD:	PRT:	233 AA.
AC	064373;	060657;	060658;	061338;	
DT	01-NOV-1997	(Rel. 35,	Created)		
DT	01-NOV-1997	(Rel. 35,	Last sequence update)		
DT	15-MAR-2004	(Rel. 43,	Last annotation update)		
DE	Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).				
DN	BCI2L1 OR BCL2L OR BCLX.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCB1	Taxid=10090;	[1]		
RN					
RP	SEQUENCE FROM N.A.				
RC	STRAIN=2A4B;				
RL	Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;				
RN	Submitted (MAR-1995) to the EMBL/GenBank/DDB databases.				
RP	[2]				
RC	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).				
RN	STRAIN=C57BL/6;				
RX	MEDLINE=95331139;				
RA	Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,				
RA	Thompson C.B., Nunez G.;				
RT	"bcl-xL is the major bcl-x-mRNA form expressed during murine				
RT	development and its product localizes to mitochondria."				
RL	Development 120:3033-3042(1994).				
RP	[3]				
RC	SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELT-TM)).				
RN	TISSUE=Pre-B cell;				
RX	MEDLINE=95052604;				
RA	Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;				
RT	"Cloning and molecular characterization of mouse bcl-x in B and T				
RT	lymphocytes."				
RL	J. Immunol. 153:4388-4398(1994).				
RN	[4]				
RC	SEQUENCE FROM N.A. (ISOFORM X(BETA)).				
RN	STRAIN=C57BL/6 X CBA;				
RX	MEDLINE=98051053;				
RA	Yang X.-P., Weber G.F., Cantor H.;				
RT	"A novel Bcl-x isoform connected to the T cell receptor regulates				
RT	apoptosis in T cells"				
RL	Immunity 7:629-639(1997).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97289584;				
RA	Grillot D.A., Gonzalez-Garcia M., Ekherse D., Duan L., Inohara N.,				
RT	Onha S., Seidin M.F., Nunez G.;				
RT	"Genomic organization, promoter region analysis, and chromosome				
RL	localization of the mouse bcl-x gene."				
CC	J. Immunol. 158:4750-4757(1997).				
CC	-I- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-				
CC	apoptotic activity is inhibited by association with SIVA isoform				
CC	1. Inhibits activation of caspases (By similarity). Appears to				
CC	regulate cell death by blocking the voltage-dependent anion				
CC	channel (VDAC) by binding to it and preventing the release of the				
CC	caspase activator. Cytochrome c, from the mitochondrial membrane.				
CC	The Bcl-X(S) isoform promotes apoptosis.				
CC	-I- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By				
CC	similarity). Heterodimerization with BAX does not seem to be				
CC	required for anti-apoptotic activity (By similarity). Isoform Bcl-				
CC	X(L) binds to Siva isoform 1 (By similarity).				
CC	-I- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear				
CC	envelope for Bcl-X(L). Cytoplasmic for Bcl-X(delta-TM).				
CC	-I- ALTERNATIVE PRODUCTS:				
CC	Name=BCLX-X(L);				
CC	Event=Alternative splicing; Named isoforms=4;				

CC		Isoid=O64373-1; Sequence=Displayed;
CC	Name=BCL-X(S);	
CC	Isoid=O64373-2; Sequence=VSP_000517;	
CC	Name=BCL-X(beta);	
CC	Isoid=O64373-3; Sequence=VSP_000518;	
CC	Name=BCL-X(delta-TM);	
CC	Isoid=O64373-4; Sequence=VSP_000519;	
CC	-1 TISSUE SPECIFICITY: Widely expressed, with highest levels in the brain, thymus, bone marrow, and kidney. Bcl-X(L) and Bcl-X(delta-TM) expression is enhanced in B and T lymphocytes that have been activated.	
CC	-1 DEVELOPMENTAL STAGE: Bcl-X(beta) is expressed in both embryonal and postnatal tissues, whereas Bcl-X(L) is predominantly found in postnatal tissues.	
CC	-1 DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.	
CC	-1 PPM: Proteolytically cleaved by caspases during apoptosis (By similarity).The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).	
CC	-1 SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.	
CC	-1 SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.	
CC	-1 SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.	
CC	-1 SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.	
CC	-1 SIMILARITY: Belongs to the Bcl-2 family.	
CC	-----	
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .	
DR	EMBL; X83574; CAAS8557.1; -	
DR	EMBL; L35049; AAAS1039.1; -	
DR	EMBL; L35048; AAA51040.1; -	
DR	EMBL; U10102; AAA82174.1; -	
DR	EMBL; U10101; AAA82173.1; -	
DR	EMBL; U10100; AAA82172.1; -	
DR	EMBL; U51279; AAC53460.1; -	
DR	EMBL; U78031; AAB96681.1; -	
DR	EMBL; U78030; AAB96681.1; JOINED.	
DR	PIR; I49055; I49055.	
DR	PIR; I49056; I49056.	
DR	PIR; I49057; I49057.	
DR	HSSP; PS3563; IAP3.	
DR	MGI; MGI:88139; Bcl2l.	
DR	InterPro; IPRO00712; Bcl2_BH.	
DR	InterPro; IPRO03093; Bcl2_BH4.	
DR	InterPro; IPRO02475; Bcl2_family.	
DR	InterPro; IPRO04725; Bcl2_reg.	
DR	Pfam; PF00452; Bcl-2; 1.	
DR	Pfam; PF02180; BH4; 1.	
DR	SMART; SMO0337; BCL; 1.	
DR	SMART; SMO0265; BH4; 1.	
DR	TIGRFAMs; TIGR00865; bcl-2; 1.	
DR	PROSITE; PSS0062; BCL2_FAMILY; 1.	
DR	PROSITE; PS01080; BH1; 1.	
DR	PROSITE; PS01258; BH2; 1.	
DR	PROSITE; PS01259; BH3; 1.	
DR	PROSITE; PS01260; BH4_1; 1.	
DR	PROSITE; PSS0063; BH4_2; 1.	
KW	Apopltosis; Mitochondrion; Alternative splicing; Transmembrane.	
FT	DOMAIN	4 .. 24 BH4.
FT	DOMAIN	86 .. 100 BH3.
FT	DOMAIN	129 .. 148 BH1.
FT	DOMAIN	180 .. 195 BH2.
FT	TRANSMEM	210 .. 226 POTENTIAL.
FT	VARSPLIC	126 .. 188 Missing (in isoform BCU-X(s)). /Frtid:VSP_000517
FT	VARSPLIC	189 .. 233 DTFYDLYGNNAASRSKGRFRNRPFLTGMYAGVLLGLSLFSRK -> VRTPLVCPLACVLSLLCHP (in isoform

FT			BCL-X(beta)}.
FT		/FTID=VSP_000518-	
FT	VANAPLIC	194	LYGNNAABESRRGQERFNRNFLTGMTVAGVVLISLFSRK
FT		233	-> GHDGCMCGSAGLTLOSSEVTRH (in isoform
FT			BCL-X(delta-TM)).
FT			/FTID=VSP_000519.
SQ	SEQUENCE	233 AA; 26132 MW;	24D2AC75887E072E CRC64;
	Query Match	42.5%;	Score 428.5; DB 1; Length 233;
	Best Local Similarity	41.3%;	Pred. No. 2.9e-31;
	Matches	93; Conservative	22; Mismatches 57; Indels 53; Gaps 4
Oy		11	RALVADPFYGYKLROGY-----V 28
Dd		6	RELVDVFSLYSKLSQNGYSMSQSDVEENRTAPEETEARETPPSAINGNPHMLADSPAV 65
Oy		29	CGAGPGECPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAOLHTVPGSAQQERT 80
Dd		66	NGA-TGHSSSLDAREVIMAAVKQALREAGDFELRYRRAFSDLTNSQLHITGTGAQSPE 124
Oy		81	QVSDELFGCGPNMGRLVAFPFVFGAALCAESVNKENEPYGVQVQDMVAYLEFLRLADWHS 140
Dd		125	QVNELEFPDGQVMGRIVAFPFSGCALCVESVDKEQVSVRSIASMMATYNLDHELPWIOE 184
Oy		141	SCGNAEFITALYGDDGLTEEARLRRE--GNMASRVTLTGAGVALGAL 183
Dd		185	NGMDTFVDLYGNNAABESRRGQERFNRFVTGMTVAGVVLIGSL 229
<hr/>			
RESULT 7			
BCLX_RAT			
ID	BCLX_RAT	STANDARD:	PRT: 233 AA
AC	P53563; P70613; P70614; Q62678; Q62836; Q64087; Q64128;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).		
CN	BCL2L1 OR BCL2L OR BCLX.		
OS	Rattus norvegicus (rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).		
RC	TISSUE=Brain;		
RA	Michaeilidis T.M.;		
RL	Submitted (DEC-1994) to the EMBL/genbank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Weeslingh S.L., David G.L., Choi S., Velliona M., Hardwick J.M.;		
RL	Submitted (JUN-1995) to the EMBL/genbank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).		
RC	TISSUE=Thymus;		
RA	MEDLINE=96278736; PubMed=8662675;		
RL	"Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;		
RT	An additional form of rat Bcl-x, Bcl-xbeta, generated by an		
RT	unspliced RNA, promotes apoptosis in promyeloid cells.";		
J.	Biol. Chem. 271:13258-13265(1996).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).		
RC	STRAIN=Sprague-Dawley; TISSUE=Ovary;		
RX	MEDLINE=95129487; PubMed=782856;		
RA	Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;		
RT	"Expression of members of the bcl-2 gene family in the immature rat		
RT	ovary: equine chorionic gonadotropin-mediated inhibition of granulosa		
RT	cell apoptosis is associated with decreased bax and constitutive		
bcl-2	and bcl-xlong messenger ribonucleic acid levels.";		
Endocrinology	136:232-241(1995).		
RN	[5]		
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).		
RX	MEDLINE=98010630; PubMed=9346956;		

RA Morikawa K.;  
RA Arimoto M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,  
RA "Crystal structure of rat Bcl-XL. Implications for the function of  
RT the Bcl-2 protein family.",  
RL J. Biol. Chem. 272:27886-27892 (1997).  
CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-  
CC apoptotic activity is inhibited by association with SIVA isoform  
CC 1. Inhibits activation of caspases (By similarity). Appears to  
CC regulate cell death by blocking the voltage-dependent anion  
CC channel (VDAC) by binding to it and preventing the release of the  
CC caspase activator, cytochrome c, from the mitochondrial membrane.  
CC The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.  
CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
CC similarity). Heterodimerization with BAX does not seem to be  
CC required for anti-apoptotic activity (By similarity). Isoform Bcl-  
CC X(L) binds to SIVA isoform 1 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear  
CC envelope (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=Bcl-X(L);  
CC IsoId=P53563-1; Sequence=Displayed;  
CC Name=Bcl-X(S);  
CC IsoId=P53563-2; Sequence=VSP\_000520;  
CC Name=Bcl-X(beta);  
CC IsoId=P53563-3; Sequence=VSP\_000521;  
CC -1- TISSUE SPECIFICITY: Expressed in most tissues. Bcl-X(beta) is  
CC specifically expressed in cerebellum, heart, and thymus. In the  
CC ovary, the predominant form is Bcl-X(L), with a small but  
CC detectable level of Bcl-X(S).  
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
CC The BH1 and BH2 domains are required for both heterodimerization  
CC with other Bcl2 family members and for repression of cell death.  
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
CC activity (By similarity).  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -----  
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CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
CC -----  
CC EMBL; X82537; CAAS7886.1; -;  
DR EMBL; X82537; CAAS7887.1; -;  
DR EMBL; U10579; AAL19257.1; -;  
DR EMBL; U72350; AAB17353.1; -;  
DR EMBL; U72349; AAB17352.1; -;  
DR EMBL; U34863; AAA77686.1; -;  
DR EMBL; S76513; AAC60701.2; ALT\_INIT.  
DR EMBL; S78284; AAC60702.1; -;  
DR PIR; I67431; I67431.  
DR PIR; S51761; S51761.  
DR PDB; 1AF3; 07-JUL-97.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 KM Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KM 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 FT VAAPPLIC 126 188 Missing (in isoform Bcl-X(S)).  
 FT VAAPPLIC 189 233 /FtId=VSP\_000520.  
 FT VAAPPLIC 189 233 DTPVDLYGNNAASRGQERFNWFLTGMTVAGVLLGSL  
 FT PSRK -> VRTTLPVCPVLCVLSVETPCFMGSMVVED  
 FT IDSGDIPGL (in isoform Bcl-X(beta)).  
 FT /FtId=VSP\_000521.  
 FT R -> Q (IN REF. 1).  
 FT F -> S (IN REF. 2).  
 FT A -> E (IN REF. 2).  
 FT I -> L (IN REF. 4).  
 FT A -> V (IN REF. 4).  
 FT FF -> SS (IN REF. 4).  
 FT A -> T (IN REF. 4).  
 FT A -> P (IN REF. 4).  
 FT HELIX 4 19  
 FT TURN 20 21  
 FT TURN 25 28  
 FT TURN 82 83  
 FT HELIX 84 100  
 FT HELIX 106 112  
 FT TURN 116 117  
 FT HELIX 120 127  
 FT HELIX 128 131  
 FT TURN 132 133  
 FT HELIX 137 156  
 FT TURN 157 158  
 FT TURN 160 161  
 FT HELIX 162 177  
 FT TURN 178 184  
 FT HELIX 179 184  
 FT TURN 185 186  
 FT HELIX 187 195  
 SQ SEQUENCE 233 AA; 26158 MW; 2B62B6C3864BC8F CRC64;  
 Query Match 42.5%; Score 428.5; DB 1; Length 233;  
 Best Local Similarity 41.3%; Pred. No. 2.9e-31;  
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;  
 QY 11 RAIVADPVGKLRKQGY-----V 28  
 DB 6 RELVVDPLSTYKLSQKGYSWQSQSDVENRTAPEETEPEERTPSAINGNPSMHLADSPAV 65  
 QY 29 CGAGPGCGPAD-----PLHQAMRAAGDEFETFRFRTSDLAQLHTVPGSAQGRFT 80  
 DB 66 NGA-TGHSSTDAEVEVPMVAVKQALREAGDEFELRYRRAASDLSQHLTPGTAQSF 124  
 QY 81 QVSDLEFGQGNMGLVAFFVFGAALCAESYNKMEPLVGVQDVMVALETSLADWTHS 140  
 DB 125 QVNVLEFRDGVNMRIVAFSFGALCVESYDKEMQVLSRIASMMATYLNLDHLEPWIOE 184  
 QY 141 SGGNAEFALYGDGALREARLR--GNWASVRYLVGAVALLGL 183  
 DB 185 NGWMDTFVDLYGNNAASRGQERFNWFLTGMTVAGVLLGSL 229

GN BCL2L1 OR BCL2L OR BCLX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
 RX MEDLINE=93364977; PubMed=8358789;  
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 Tuika L.A., Mao X., Nunez G., Thompson C.B.;  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 of apoptotic cell death."  
 RL Cell 74:597-608(1993).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).  
 RA Inohara N., Ohta S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A. (ISOFORM X(L)).  
 RX TISSUE=lung;  
 MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein W.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,  
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [4]  
 RP MUTAGENESIS OF GLY-138 AND HETERODIMERIZATION.  
 RX MEDLINE=95372373; PubMed=7644501;  
 RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,  
 Korsmeyer S.J.;  
 RT "Multiple Bcl-2 family members demonstrate selective dimerizations  
 with Bax."  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).  
 [5]  
 RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.  
 RX MEDLINE=96170038; PubMed=859636;  
 RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,  
 Korsmeyer S.J.;  
 RT "Bax-independent inhibition of apoptosis by Bcl-XL."  
 RL Nature 379:554-556(1996).  
 [6]  
 RP INTERACTION WITH SIVA.  
 RX MEDLINE=22008092; PubMed=12011449;  
 RA Wu L., Chu F., Cheng Y., Sun X., Borthakur A., Ramarao M., Pandey P.,  
 Xu M., Schlossman S.F., Prasad K.V.S.;  
 RT "Siva-1 binds to and inhibits Bcl-X(L)-mediated protection against UV  
 radiation-induced apoptosis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).  
 [7]  
 RP STRUCTURE BY NMR OF 1-209.  
 RX MEDLINE=97172562; PubMed=9020082;  
 RA Sactier M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,  
 Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mann A.J.;  
 RA Thompson C.B., Fesik S.W.;  
 RT "Structure of Bcl-XL-Bak peptide complex: recognition between  
 regulators of apoptosis."  
 RL Science 275:983-986(1997).

[8]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.  
 RP MEDLINE=96256675; PubMed=8692274;  
 RX Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,  
 RA Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,  
 RA Ng S.L., Fesik S.W.;  
 RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed  
 cell death";  
 RL Nature 381:335-341 (1996).  
 [9]  
 RN CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
 RP MEDLINE=98118550; PubMed=9435230;  
 RX Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
 RA Takahashi A., Kaestan M.B., Griffin D.E., Earnshaw W.C., Vellutina M.A.,  
 RA Harwick J.M.;  
 RT "Modulation of cell death by Bcl-XL through caspase interaction.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-  
 apoptotic activity is inhibited by association with SIVA isoform  
 1. Inhibits activation of caspases (by similarity). Appears to  
 regulate cell death by blocking the voltage-dependent anion  
 channel (VDAC) by binding to it and preventing the release of the  
 caspase activator, cytochrome c, from the mitochondrial membrane.  
 CC The Bcl-X(S) isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 apoptotic activity. Isoform Bcl-X(L) binds to SIVA isoform 1.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear  
 envelope (by similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=Bcl-X(L);  
 CC IsoId=Q07817-1; Sequence=Displayed;  
 CC Name=Bcl-X(S);  
 CC IsoId=Q07817-2; Sequence=VSP\_000515;  
 CC Name=Bcl-X(beta);  
 CC IsoId=Q07817-3; Sequence=VSP\_000516;  
 CC -1- TISSUE SPECIFICITY: Bcl-X(S) is expressed at high levels in cells  
 that undergo a high rate of turnover, such as developing  
 lymphocytes. In contrast, Bcl-X(L) is found in tissues containing  
 long-lived postmitotic cells, such as adult brain.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 activity.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
 CC -----  
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 CC -----  
 DR EMBL, Z23116; CAAB0662.1; -  
 DR EMBL, Z23115; CAAB0661.1; -  
 DR EMBL, U72398; AAB17354.1; -  
 DR EMBL, BC019307; AAH19307.1; -  
 DR PIR, B47537; B47537.  
 DR PIR, J80203; J80203.  
 DR PDB, 1BXL; 29-OCT-97.  
 DR PDB, 1LXL; 21-APR-97.  
 DR PDB, 1MAZ; 21-APR-97.  
 DR PDB, 1G5J; 07-FEB-01.  
 DR PDB, 1G5M; 21-MAR-01.  
 DR PDB, 1G5H; 13-JUN-01.

DR Genew; HGNC:992; BCL2L1.  
 DR MIM: 600039; -  
 DR GO; GO:0005739; C:mitochondrion; TAS.  
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
 DR GO; GO:0006916; F:anti-apoptosis; TAS.  
 DR GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.  
 DR GO; GO:0008634; P:negative regulation of survival gene products; TAS.  
 DR InterPro; IPR001072; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRfam; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS00663; BH4\_2; 1.  
 DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KW 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT 86 100 BH3.  
 FT 129 148 BH1.  
 FT 180 195 BH2.  
 FT 210 226 POTENTIAL.  
 FT 210 226 CLEAVAGE (BY CASPASE-1).  
 FT SITE 61 62 Missing (in isoform Bcl-X(S)).  
 FT VARSPPLIC 126 188 /FTId=VSP\_000515.  
 FT VARSPPLIC 189 233 DTFVELYGNMAAESRKGGRFNNRFLTGMVAVGLLGS  
 FT VARSPLIC 189 233 FSRK -> YRKRLVCPRLSLASGCSFALLLLYFLLCMTI  
 FT VGVVDS (in isoform Bcl-X(beta)).  
 FT /FTId=VSP\_000516.  
 FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY  
 FT CASPASE-3.  
 FT FRD->VRA: NO HETERODIMERIZATION WITH BAX.  
 FT VNM->ALL: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT MUTAGEN 138 140 G->A: NO HETERODIMERIZATION WITH BAX.  
 FT 138 138 G->E: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 148 148 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT 176 176 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT MUTAGEN 188 189  
 Query Match 42.4%; Score 427.5; DB 1; Length 233;  
 Best Local Similarity 41.3%; Pred. No. 3,6e-31;  
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;  
 QY 11 RALVADPVGVYKLRQKGY-----Y 28  
 DB 6 RELVVDPLSTYKLSQSGVMSQSDVEENRTEAPEGTESEMETPSALNGNPSWHLADSPAV 65  
 QY 29 CGAGGGBPAD-----PLHQMRAAGDEFERFRRTSDLAQCHVTPGSGQQRT 80  
 DB 66 NGA-TGSHSSLDAREVIMPAVKQALREAGDEFELRYRRASDLSQLHTIPGTAYQSE 124  
 QY 81 QVSDLEFQGGPWGRLVAFVVGALCAESYKMEKPELVGOVDMVAVYLETRLADWTHS 140  
 DB 125 QVNELEFRDGVNMGWIVAFVFSFGALCVESVDKENVYSKRAMMATYLNDDHLEPWIGE 184  
 QY 141 SGMAEFALYDGDALFEARRLRE--GNWASRYTLTGAVALLGAL 183  
 DB 185 NCGMDTFVELYGNMAAESRKGGRFNNRFLTGMVAVGLLGS 229  
 RESULT 9  
 BCL2\_CHICK  
 ID\_BCL2\_CHICK STANDARD; PRT; 233 AA.

AC 000709:  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 in a variety of tissues including lymphoid and neuronal organs in  
 adult and embryo.";  
 RT Nucleic Acids Res. 20:4187-4192 (1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell lymphoma;  
 RX MEDLINE=92379084; PubMed=1511008;  
 RA Carale-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;  
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
 homologue of the Bcl-2 oncoprotein.";  
 RL Blochm. Biophys. Acta 1132:109-113 (1992).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2  
 domains, and is necessary for anti-apoptotic activity (by  
 similarity). Also interacts with APAF-1 and Raf-1 (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,  
 kidney, heart, ovary and brain, with the highest levels in the  
 thymus. In the embryo, highly levels expressed in all tissues with  
 high levels in the bursa of Fabricius.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 for interaction with Raf-1 (by similarity).  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D11382; BAA01978.1; JOINED.  
 DR EMBL: D11381; BAA01978.1; JOINED.  
 DR EMBL: Z11961; CAA78018.1; -.  
 DR PIR: A37332; A37332.  
 DR PIR: S24390; S24390.  
 DR HESP: Q07817; IMAZ.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion.  
 RN DOMAIN 10  
 FT FT 87 101 BH3.  
 FT DOMAIN 130 149 BH1.  
 FT DOMAIN 181 196 BH2.  
 FT TRANSMEM 208 228 POTENTIAL.  
 FT FT 64 64 E -> S (IN REF. 2).  
 FT CONFLICT 67 82 GSAASEVPPAEGRRP -> ARLLVRCPLRGCA  
 FT CONFLICT 121 121 H -> T (IN REF. 2).  
 FT CONFLICT 139 139 G -> V (IN REF. 2).  
 SQ SEQUENCE 233 AA; 25687 MM; 525255ACB64C3D CRC64;  
 Query Match 42.0%; Score 423.5; DB 1; Length 233;  
 Best Local Similarity 38.0%; Pred. No. 8.2e-31;  
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;  
 QY 9 DTRALVADFPVGYKLRQGYVCGAG-----PGSGPAADP----- 41  
 DB 10 DNRSLVLYHYKLSQGYMAAGEDRPPVPAAPAAVAAGASHHREPPGSA 69  
 QY 42 -----LHQMRAAGDEFETFRFTSDLAQAHVTPGSAQOQFTQVSD 84  
 DB 70 AASVPPAEGIRPAPPGVHLALRQAGDEFRRYDRDRQSGQLHPTFHAGFVAIVE 129  
 QY 85 ELFGGNNMGLVAFVFGAALCAESVKNEMEPVGVQVDMVAVYLETRLADWTHSSGCV 144  
 DB 130 ELFGDGVNMGRVIAVFFFGVGMCVESVNRMSPLVDNIATMTETLYNRHLNWIQDNGCV 189  
 QY 145 AEFPAALGDGALBEARLRSGNMAVSRTVLTGVALGALVYVGAFFPASK 193  
 DB 190 DAFELVGN-----SMRPLPFGFWSLTKTILS-LVLVAGCITLGAYLGHK 233  
 RESULT 10  
 BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 ID BCL2\_BOVIN  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RX MEDLINE=98162580; PubMed=9501056;  
 RA Reyes R.A., Cockerell G.L.;  
 RT "Increased ratio of bcl-2/bax expression is associated with bovine  
 leukemia virus-induced leukemogenesis in cattle.";  
 RL Virology 242:184-192 (1998).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (APAF-1) (by similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2

domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RA-F-1 and TP53BP2 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).  
 -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RA-F-1 (By similarity).  
 -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 -1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).  
 -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 -1- SIMILARITY: Belongs to the Bcl-2 family.  
 -----  
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 -----  
 EMBL: U92434; AAB5319.1; -.  
 DR HSPB; O07817; 1MAZ.  
 DR Interpro; IPR000712; Bcl2\_BH.  
 DR Interpro; IPR003093; Bcl2\_BH4.  
 DR Interpro; IPR002475; Bcl2\_family.  
 DR Interpro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRfam; TIGR00865; bcl2\_2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 64 68 POLY-PRO.  
 FT DOMAIN 69 72 POLY-ALA.  
 FT DOMAIN 83 97 BH3.  
 FT DOMAIN 126 145 BH1.  
 FT DOMAIN 177 192 BH2.  
 FT TRANSMEM 202 223 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT SEQUENCE 229 AA; 25099 MW; AD1DD0AF9EFP1LD CRG64;

Query Match 41.2%; Score 415.5; DB 1; Length 229;  
 Best Local Similarity 38.2%; Pred. No. 4.2e-30;  
 Matches 86; Conservative 35; Mismatches 59; Indels 45; Gaps 5;

QY 9 DRRRAVADVGVKLRKGVVCGAG-----PGF----- 35  
 DB 10 DRRRAVADVGVKLRKGVVCGAG-----PGF----- 35  
 QY 36 ---GPAAD---LHQAAPAGDEFTFRFSDIAQLVTPGSAOCRFQVSDLEFQ 88  
 DB 70 AAAGPAPSPVPVHLTLAQAGDDFSRRYTRDPAEMSSQHLTPFAERERFATVVELEFR 129

QY 89 GGPWNGRLVAFVFCALCAESVKNKEPVLGVQVDMWVAYLETRLADIMHSSGGMAEFT 148  
 DB 130 DGVNMRVIAFFEPFGVGVCSVNVREMSPLVDSIALMWTETYLNRHLHWIDQNGMDAFV 189  
 QY 149 ALYGDALBEARRLRNEGMAVSRVTLGVALGALVTVGAFPAASK 193  
 DB 190 ELYG---FSMRPLFDPSMLSLKLLSLAL-VGACITLGAYLGHK 229  
 RESULT 11  
 ID BCL2 RAT STANDARD; PRT; 236 AA.  
 AC P49950; 062837; 064032;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=94193015; PubMed=8144041;  
 RA Sato T., Irie S., Krajewski S., Reed J.C.;  
 RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";  
 RL Gene 140:291-292(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
 RX MEDLINE=95129487; PubMed=7828536;  
 RA Tilly J.L., Tilly K.I., Kenton M.W., Johnson A.L.;  
 RT "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xl-messenger ribonucleic acid levels.";  
 RL Endocrinology 136:232-241(1995).  
 RN [3]  
 RP SEQUENCE OF 19-172 FROM N.A.  
 RX MEDLINE=95059917; PubMed=7969891;  
 RA Castrén E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H., Lindholm D.;  
 RT "bcl-2 messenger RNA is localized in neurons of the developing and adult rat brain.";  
 RL Neuroscience 61:165-177(1994).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RA-F-1 and TP53BP2 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RA-F-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and

occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dpphosphorylated by protein phosphatase 2A (PP2A) (By similarity).

-1- PPM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-1- SIMILARITY: Belongs to the Bcl-2 family.

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DR EMBL: L14680; AAA53662.1; -

DR EMBL: U34964; AAA77687.1; -

DR PIR: I53744; I53744.

DR PIR: I67432; I67432.

DR HSP: Q07817; IMAZ.

DR InterPro: IPR000172; Bcl2\_BH.

DR InterPro: IPR003093; Bcl2\_BH4.

DR InterPro: IPR002475; Bcl2\_family.

DR InterPro: IPR004725; Bcl2\_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SMO0337; BCL; 1.

DR SMART: SMO0265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS50063; BH4\_2; 1.

DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

FT DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT CONFLICT 42 42 A -> R (IN REF. 2).

FT CONFLICT 157 157 E -> G (IN REF. 1).

FT CONFLICT 164 164 S -> Y (IN REF. 2).

FT CONFLICT 212 212 L -> Q (IN REF. 2).

FT SEQUENCE 236 AA; 26622 MW; E7686CB9071A872A CRC64;

Query Match 40.9%; Score 413; DB 1; Length 236;  
Best Local Similarity 36.2%; Pred. No. 7,3e-30;  
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADPVGYKLRQKY----- 27

DB 10 DNRIFVMKVIHYKLSQSGVEMDTGDEDSAPLAAPTPGIFSGFQESNRTPAVHDTAART 69

QY 28 -----VCGAGPGSGPADPLHGMRAAGDEFRTFRFTFDLAAQCLHTPGSGAQPRTPQ 81

DB 70 SPLRLVANNAGPASPVPVVLTLRRGDDFSRRYRDFEWSQQLTLFTFARGRPAT 129

QY 82 VSDRLFGCGPMGRVLVAFVFGALCAESVKNEMEPVLGVQODMMVAVLETFLADWIHS 141

DB 130 VVEELFRGCVWGRIVAFERFGVWCVSVREMSPLVDNIALMTETLNLHHTWIDN 189

142 GGNAPFTALYGDGALFEARLRREGNMAVETVLGVALGALVTGAFAPFASK 193

DB 190 GGNDAFVELVIG-----PSMRPLPDSWLSKTLISLAL-VACITLGVLYGKH 236

RESULT 12

BCL2\_MOUSE STANDARD; PRT; 236 AA.

ID BCL2\_MOUSE

AC P10417; P10418;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apoptosis regulator Bcl-2.

GN BCL2 OR BCL-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

[1]

SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

RC STRAIN=BAB/c; TISSUE=Liver;

RX MEDLINE=87187643; PubMed=3032455;

RA Negri M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;

RT "Molecular analysis of bcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";

RL Cell 49:455-463(1987).

RN [2]

RN REVISIONS TO 221-222.

RX MEDLINE=92375724; PubMed=1508712;

RA Eguchi Y., Ewert D.L., Tsujimoto Y.;

RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

RL Nucleic Acids Res. 20:4187-4192(1992).

RN [3]

RN PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.

RX MEDLINE=92727291; PubMed=9115213;

RA Ito T., Deng X., Carr B., May W.S. Jr.;

RT "Bcl-2 phosphorylation required for anti-apoptosis function.";

RL J. Biol. Chem. 272:11671-11673(1997).

RN [4]

RN DEPHOSPHORYLATION BY PP2A.

RX MEDLINE=99069407; PubMed=9852076;

RA Deng X., Ito T., Carr B., Mundy M., May W.S. Jr.;

RT "Reversible phosphorylation of Bcl2 following interleukin 3 or bryostatine 1 is mediated by direct interaction with protein phosphatase 2A\*.";

RL J. Biol. Chem. 273:34157-34163(1998).

CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).

CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Interacts with TP53BP2 (By similarity). Also interacts with APAF-1 and RAIF-1.

CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;

CC Name=Alpha;

CC IsoId=P10417-1; Sequence=Displayed;

CC Name=Beta;

CC IsoId=P10417-2; Sequence=VSP\_000513;

CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.

CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAIF-1.

CC -1- PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation

on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A).

-1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

-1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-1- SIMILARITY: Belongs to the Bcl-2 family.

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EMBL: L11532; AAA37282.1; -  
 DR EMBL: M16506; AAA37282.1; JOINED.  
 DR EMBL: M16506; AAA37281.1; -  
 DR PIR: B25960; TVMSB1.  
 DR HSSP: Q07817; TMAZ.  
 DR MGD: MGI:88138; Bcl2.  
 DR GO: GO:0005829; C:cytosol; IDA.  
 DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.  
 DR GO: GO:0005515; F:protein binding; IPI.  
 DR GO: GO:0006915; F:apoptosis; IDA.  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR InterPro: IPR003093; Bcl2-BH4.  
 DR InterPro: IPR002475; Bcl2 family.  
 DR InterPro: IPR004725; Bcl2-reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAM: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00682; BCL2 family; 1.  
 DR PROSITE: PS01080; BCL2 family; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1; 1.  
 DR PROSITE: PS00663; BH4 2; 1.  
 KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Phosphorylation.

KV Phosphorylation.

FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC).  
 FT VARSPLIC 193 236 DAFVEYLGSMPPLFDFSWLSKTLTSLALVGACITLGLAYL  
 FT /FTID=VSP 000513.  
 FT /FTID=VSP 000513.  
 SQ SEQUENCE 236 AA; 26425 MW; AA85EF6B0766BE0A CRC64;

Query Match 40.8%; Score 412; DB 1; Length 236;  
 Best Local Similarity 37.5%; Pred. No. 8; 9e-30;  
 Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRATADVGVKLRKGVVCGAG-----PG----- 34  
 DB 10 DNRRLVWKTHYKLSRGTEWMDGADAAPLGAAPPGGLFSPQPSNPVAVHREMAART 69  
 QY 35 -----EGPAADP-----LHQAMRAAGDEFEFRRTFTSDLAQHTVPGSAQOQRTQ 81  
 DB 70 SPLRLVATAGPALSLVPPCVHLTLRADDPSRRYRRRPFAMSSQLHLTPFARGRFAT 129

QY 82 VSEDFGCGPMWGRVAFVFFGALCAESVKNEMPLVGQVQDMMVAYLETRADWHS 141  
 DB 130 VVEELFRGVANWGRVAFVFFGCGVNCVSVREMSPLVDNIALMWTEVLNRLHWMQDN 189  
 QY 142 GGMVAFETALYGDGALGEARRLREGNWSVRIVLTGVALGALVTVGAFPAK 193  
 DB 190 GGMVAFVETLYG----PSMRPLFDFSWLSKTLTSLAL-VGACITLGLAYLGHK 236

RESULT 13  
 BCL2 HUMAN STANDARD; PRT; 239 AA.  
 AC P10415; P10416; Q13842; Q16197;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).  
 RX MEDLINE=86259760; PubMed=3523487;  
 RA Tsujimoto Y., Croce C.M.;  
 RT "Analysis of the structure, transcripts, and protein products of  
 RT bcl-2, the gene involved in human follicular lymphoma.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
 RN [2]  
 RP REVISIONS TO 96; 110 AND 237.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Swert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RX MEDLINE=87002488; PubMed=2875799;  
 RA Cleary M.L., Smith S.D., Sklar J.;  
 RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-  
 RT 2/immunoglobulin transcript resulting from the t(14;18)  
 RT translocation.";  
 RL Cell 47:19-28(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RX MEDLINE=88196071; PubMed=2834197;  
 RA Seto M., Jaeger U., Hockett R.D., Granger W., Bennett S.,  
 RA Goldman P., Korsmeyer S.J.;  
 RT "Alternative promoters and exons, somatic mutation and deregulation  
 RT of the Bcl-2-1g fusion gene in lymphoma.";  
 RL EMBO J. 7:123-131(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
 RL submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hootne R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carinci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,



RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Falley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [7]  
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS  
RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.  
RX MEDLINE=92096610; PubMed=1339299;  
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;  
RT "Frequent incidence of somatic mutations in translocated BCL2  
RT oncogenes of non-Hodgkin's lymphomas.";  
RL Blood 79:229-237(1992).  
RN [8]  
RP SUBCELLULAR LOCATION.  
RX MEDLINE=91066924; PubMed=2250705;  
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;  
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks  
RT programmed cell death.";  
RL Nature 348:334-336(1990).  
RN [9]  
RP MUTAGENESIS.  
RX MEDLINE=94239528; PubMed=8183370;  
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;  
RT "BHL1 and BHL2 domains of Bcl-2 are required for inhibition of  
RT apoptosis and heterodimerization with Bax.";  
RL Nature 369:321-323(1994).  
RN [10]  
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
RX MEDLINE=98057466; PubMed=9395403;  
RA Cheng E.H.-Y., Kitzberg D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
RA Ueno K., Hardwick J.M.;  
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";  
RL Science 278:1966-1968(1997).  
RN [11]  
RP INTERACTION WITH TP53BP2.  
RX MEDLINE=96251339; PubMed=8668206;  
RA Namovskii L., Cleary M.L.;  
RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes  
RT cell cycle progression at G2/M.";  
RL Mol. Cell. Biol. 16:3884-3892(1996).  
RN [12]  
RP REVIEW ON PHOSPHORYLATION.  
RX MEDLINE=21260650; PubMed=11368354;  
RA Ruvolo P.P., Deng X., May W.S.;  
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";  
RL Leukemia 15:515-522(2001).  
RN [13]  
RP PHOSPHORYLATION BY ASK1/JNK1.  
RX MEDLINE=20036804; PubMed=10567572;  
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
RT protein kinase pathway normally activated at G(2)/M.";  
RL Mol. Cell. Biol. 19:8469-8478(1999).  
RN [14]  
RP FUNCTION: Suppresses apoptosis in a variety of cell systems  
RP including factor-dependent lymphohematopoietic and neural cells.  
RP Regulates cell death by controlling the mitochondrial membrane  
RP permeability. Appears to function in a feedback loop system with  
RP caspases. Inhibits caspase activity either by preventing the  
RP release of cytochrome c from the mitochondria and/or by binding to  
RP the apoptosis-activating factor (Apaf-1).  
RN [15]  
RP SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
RP BCL-X(L). Heterodimerization with BAX requires intact BHL and BHL2  
RP domains, and is necessary for anti-apoptotic activity (by  
RP similarity). Also interacts with APAF-1, RAF-1 and TP53BP2.  
RN [16]  
RP SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
RP membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Alpha;  
CC IsoId=PI0415-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=PI0415-2; Sequence=VSP 000512;  
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
CC -1- DOMAIN: The BHL domain is required for anti-apoptotic activity and  
CC for interaction with Apaf-1.  
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC Dephosphorylated by protein phosphatase 2A (PP2A) (by similarity).  
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BHL domain, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol  
CC promoting further caspase activity.  
CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type  
CC II chronic lymphatic leukemia) by a chromosomal translocation  
CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene  
CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying  
CC the chromosomal translocation could be attributed to the Ig  
CC somatic hypermutation mechanism resulting in nucleotide  
CC transfections.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BHL1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BHL2) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BHL3) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BHL4) domain.  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -1- DATABASE: NAME=Atlas Gene. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.inobloggen.fr/services/chromocancer/gene/BCL2ID49.html".  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC  
CC EMBL: M13994; AAAS1813.1; ALT\_SEQ.  
CC EMBL: M13995; AAAS1814.1; ALT\_SEQ.  
CC EMBL: M14745; AAA35591.1; -.  
CC EMBL: X06487; CAA29778.1; -.  
CC EMBL: AY220759; AA026045.1; -.  
CC EMBL: BC027258; AA827258.1; -.  
CC EMBL: S72602; AAD14111.1; ALT\_SEQ.  
CC PIR: B29409; TVHUB1.  
CC PIR: C37332; TVHUB1.  
CC PDB: 1G5M; 21-MAR-01.  
CC PDB: 1GJH; 13-JUN-01.  
CC GeneW: HGNC:990; BCL2.  
CC MIM: 151430; -.  
CC DR GO: GO:0005743; C:mitochondrial inner membrane; TAS.  
CC DR GO: GO:0008189; F:apoptosis inhibitor activity; TAS.  
CC DR GO: GO:0006916; F:anti-apoptosis; TAS.  
CC DR GO: GO:0006959; P:humoral immune response; TAS.  
CC DR GO: GO:0008285; P:negative regulation of cell proliferation; TAS.  
CC DR GO: GO:000074; P:regulation of cell cycle; TAS.  
CC DR InterPro: IPR000712; BCL2\_BH.  
CC DR InterPro: IPR003093; BCL2\_BH4.  
CC DR InterPro: IPR002475; BCL2\_family.  
CC DR InterPro: IPR004725; BCL2\_reg.  
CC  
CC Query Match 40.8%; Score 411.5; DB 1; Length 229;  
CC Best Local Similarity 37.0%; Pred. No. 1e-29;  
CC Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;  
CC  
CC 9 DTRALVADPFQYKLRQKGYCGAG-----PGE----- 35



```

OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
   cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: Confers strong protection against cell death.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
   brain of mid-metamorphic to post-metamorphic tadpoles and
   adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X82461; CAA57844.1; -.
DR HSSP, Q07817; IMX2.
DR InterPro, IPR000712; Bcl2_BH.
DR InterPro, IPR003093; Bcl2_BH4.
DR InterPro, IPR002475; Bcl2_family.
DR InterPro, IPR004725; Bcl2_reg.
DR Pfam, PF00452; Bcl-2; 1.
DR Pfam, PF02180; BH4; 1.
DR SMART, SM00337; BCL; 1.
DR SMART, SM00265; BH4; 1.
DR TIGRFAMs, TIGR00865; bcl-2; 1.
DR PROSITE, PS01080; BH1; 1.
DR PROSITE, PS01258; BH2; 1.
DR PROSITE, PS00062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
KW DOMAIN
FT 101 120 BH1.
FT DOMAIN
FT 152 167 BH2.
FT TRANSMEM
FT 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFC6B6DDA4CA03 CRC64;
Qy Query Match 36.6%; Score 369; DB 1; Length 204;
Db Best Local Similarity 42.1%; Pred. No. 5.3e-26;
Matches 82; Conservative 24; Mismatches 63; Indels 26; Gaps 4;
Qy 10 TRALVADVGVKYLRLKRGIVC-----GAGPGGGRPAADPHQMR 47
Db 5 SRDLVEKRVSSKGLSG-NEACRKFSSNNPMPYLMPESTSEREGEGATGIVEEVLQALL 63
Qy 48 AAGDEFETFRPRTFSDLAALQVHTPGSAQOQRPFGVSDLEFGQGPWGRVLVAFVFGALC 107
Db 64 EATEFEFLRYQRAEFDLTSLQHLITDPTIAQOSQOVMGELFRGTWGIIVAFFSGRALC 123
Qy 108 AESVUNKEMEPVLGVQVQDMVVAVYLETRLADWHSGGMAFTALYGDGLAEARRLRE--G 165
Db 124 VESANKENTDILLPRIVQMVVVNLTLEHTLQPMWQENGCGMEAFGLYKNNAAQGRSGRPF 183
Qy 166 NWASIVRTVLTGAVALL 180
Db 184 RLRTI-VMLTGVPAL 197

```

Search completed: February 26, 2004, 11:13:30  
Job time : 20 secs

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## OM protein - protein search, using sw model

Run on: February 26, 2004, 11:10:37 / Search time 45 Seconds

(without alignments)  
1353.223 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009  
Sequence: 1 MATRPASPPDRALVADPVG.....LTGAVLALGVTAFFASK 193Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriophage:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	99.6	193	11	088996 ratius norv
2	1005	99.6	219	11	07TS60 ratius norv
3	965	95.6	193	11	08CG14 mus musculu
4	770	76.3	178	11	09CWM5 mus musculu
5	770	76.3	178	11	08CFR2 mus musculu
6	439.5	43.6	233	6	Q9MYW4 oryctolagus
7	435.5	43.2	233	11	035844 mus musculu
8	432.5	42.8	233	6	08SQ42 felis silve
9	431.5	42.8	233	6	09N1A2 sus scrofa
10	428.5	42.5	233	6	Q9MZS7 ovis aries
11	412	40.8	236	11	08BQK4 mus musculu
12	412	40.8	236	11	07TSN8 ratius norv
13	406	39.7	79	11	07TS61 ratius norv
14	401	39.2	180	6	Q9BD5 bos taurus
15	401	39.7	217	11	Q9N35 mus musculu
16	400	39.6	238	13	Q90298 brachydanio

17	398.5	39.5	180	6	Q9BDX7 bos taurus
18	398	39.4	236	11	Q923R6 cricetus
19	395.5	39.2	235	6	Q8I008 felis silve
20	380.5	37.7	284	11	Q7S62 ratius norv
21	374.5	37.1	188	11	Q9QMX2 mus musculu
22	374.5	37.1	235	11	Q35843 mus musculu
23	372.5	36.9	188	4	Q9H1R6 homo sapien
24	371	36.8	204	13	Q90ZH2 xenopus lae
25	365.5	36.2	153	6	Q7YR66 canis famli
26	353	35.0	185	6	Q8MJ81 bos taurus
27	347	34.4	219	11	Q9N36 mus musculu
28	342.5	33.9	199	11	Q8C5P0 mus musculu
29	296	29.3	89	13	Q8UWJ1 gallus gall
30	187	18.5	209	11	Q9UK59 ratius norv
31	185	18.3	170	11	Q9WJ15 ratius norv
32	182	18.0	209	11	Q8C264 mus musculu
33	174.5	17.3	192	13	Q919N4 brachydanio
34	172.5	17.1	221	13	Q98U13 xenopus lae
35	170.5	16.9	190	4	Q8NFP3 homo sapien
36	168.5	16.7	125	4	Q9H1R5 homo sapien
37	163	16.2	235	5	Q967D2 geodia cydo
38	162	16.1	58	11	Q9R1B3 ratius norv
39	157.5	15.6	163	6	Q9MZ66 ovis aries
40	156.5	15.5	173	11	Q8K3J2 mus musculu
41	154	15.3	173	4	Q8W249 homo sapien
42	154	15.3	173	11	Q9UKL3 cervus elap
43	151	15.0	67	6	Q8MJ83 felis silve
44	149	14.8	192	6	Q8SQ43 suberites d
45	148.5	14.7	218	5	Q9N754

## ALIGNMENTS

RESULT 1

ID 088996 PRELIMINARY; PRT; 193 AA.

AC 088996; 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Bcl-w.

GN BCL-W.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

FX MEDLINE=99292146; PubMed=1036024;

RA Hammer S., Skoglosa Y., Lindholm D.,

RT "Differential expression of bcl-w and bcl-x messenger RNA in the

RT developing and adult rat nervous system.";

RL Neuroscience 91:673-684(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

FX MEDLINE=22672518; PubMed=12787069;

RA Itoh T., Itoh A., Pleasure D.,

RT "Bcl-2-related protein family gene expression during oligodendroglial

RT differentiation.";

RL J. Neurochem. 85:1500-1512(2003).

DR EMBL; AF096291; AAC64200.1; -.

DR HSSP; Q07817; IMAZ.

DR GO; GO:0016329; F:apoptosis regulator activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR InterPro; IPR000712; Bcl2\_BH.

DR InterPro; IPR003093; Bcl2\_BH4.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 193;  
 Best Local Similarity 99.5%; Pred. No. 3.9e-81;  
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRPRT 60  
 DB 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRPRT 60  
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 120  
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 120  
 QY 121 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 180  
 DB 121 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 180  
 QY 181 GALVTGAFPAK 193  
 DB 181 GALVTGAFPAK 193

## RESULT 2

QY 07TS60 PRELIMINARY; PRT; 219 AA.  
 AC 07TS60;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE BCL-WEL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=2672518; PubMed=12787069;  
 RA Itoh T., Itoh A., Pleasure D.;  
 RT "Bcl-2-related protein family gene expression during oligodendroglial  
 differentiation";  
 RT EMBL; AY185100; AA064470.1; --  
 DR EMBL; AY185100; AA064470.1; --  
 SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 219;  
 Best Local Similarity 99.5%; Pred. No. 4.6e-81;  
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRPRT 60  
 DB 27 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRPRT 86  
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 120  
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 120  
 QY 87 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 146  
 DB 87 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 146  
 QY 121 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 180  
 DB 121 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 180  
 QY 147 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 206  
 DB 147 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 206  
 QY 181 GALVTGAFPAK 193  
 DB 207 GALVTGAFPAK 193

RESULT 3  
 O8CGL4 PRELIMINARY; PRT; 193 AA.  
 ID O8CGL4;  
 AC O8CGL4;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Bcl2-like protein 2.  
 GN BCL2L2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL; TISSUE=Skin;  
 RA Su H.-Y.;  
 RT "Extraction from neonatal mouse skin after IGF-1 stimulation."  
 RT Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY170344; AA013177.1; --  
 DR MGD; MGI:108052; Bcl2l2.  
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 SQ SEQUENCE 193 AA; 20950 MW; 258AC181816CDFA0 CRC64;

Query Match 95.6%; Score 965; DB 11; Length 193;  
 Best Local Similarity 96.4%; Pred. No. 1.4e-77;  
 Matches 186; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRPRT 60  
 DB 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETFRPRT 60  
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 120  
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDLEFGGPGWGRVAVFVFGALCAESVNKEEPLVG 120  
 QY 121 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 180  
 DB 121 QVQDMWVAVLETRLADWVHSSGMAEFTALYGDGALBEARRLRBNWNASVRTLGAVAL 180  
 QY 181 GALVTGAFPAK 193  
 DB 181 GALVTGAFPAK 193

## RESULT 4

QY 09CYW5 PRELIMINARY; PRT; 178 AA.  
 ID 09CYW5;  
 AC 09CYW5;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 24, Last annotation update)  
 DE Bcl2-like 2.  
 GN BCL2L2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Atkawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,  
 RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kocha H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,  
 RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hoffmann M., Hume D.A., Kamita M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaers P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,  
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohbuchi S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RT Nature 409:685-690(2001).  
 DR EMBL; AK013244; BAB28740.1; -  
 DR HSSP; Q07817; IMAZ.  
 DR MGD; MG1:108052; Bcl2l2.  
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
 DR CO; CO:0006915; P:apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 178 AA; 19147 MW; E2D4CF79528E9D7 CRC64;  
 Query Match 76.3%; Score 770; DB 11; Length 178;  
 Best Local Similarity 96.7%; Pred. No. 2.3e-60;  
 Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60  
 DB 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60  
 QY 61 FSDLAALQHLHTPGSAQGRFTQVSDLEFGGPNMGRVLFVFGALCAESYKMEPLVG 120  
 DB 61 FSDLAALQHLHTPGSAQGRFTQVSDLEFGGPNMGRVLFVFGALCAESYKMEPLVG 120  
 QY 121 QVQDMVAVLETRLDADWIHSSGGMWRRSSQL 150  
 DB 121 QVQDMVAVLETRLDADWIHSSGGMWRRSSQL 150  
 RESULT 5  
 Q8CFR2 PRELIMINARY; PRT; 178 AA.  
 AC O8CFR2; (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Bcl2-1ike 2.  
 GN BCL2L2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strauberg R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC040369; AAH40369.1; -  
 DR MGD; MG1:108052; Bcl2l2.  
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;  
 Query Match 76.3%; Score 770; DB 11; Length 178;  
 Best Local Similarity 96.7%; Pred. No. 2.3e-60;  
 Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60  
 DB 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60  
 QY 61 FSDLAALQHLHTPGSAQGRFTQVSDLEFGGPNMGRVLFVFGALCAESYKMEPLVG 120  
 DB 61 FSDLAALQHLHTPGSAQGRFTQVSDLEFGGPNMGRVLFVFGALCAESYKMEPLVG 120  
 QY 121 QVQDMVAVLETRLDADWIHSSGGMWRRSSQL 150  
 DB 121 QVQDMVAVLETRLDADWIHSSGGMWRRSSQL 150  
 RESULT 6  
 Q9MYW4 PRELIMINARY; PRT; 233 AA.  
 AC Q9MYW4; (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Bcl-X.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Knott J.C., Robertson L., James E.R.;  
 RT "Rabbit Bcl-X";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY005131; AAF88137.1; -  
 DR HSSP; P53563; IAF3.  
 DR GO; GO:0016029; C:membrane; IEA.  
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match      43.6%; Score 439.5; DB 6; Length 233;
Best Local Similarity 42.0%; Pred. No. 5,9e-31;
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADPVGYKLRQKGYC-----GAG-----PGGPPAA 39
DB 6 RELVVDPLSLYKLSQKGYSMQSFSDVEENRTEAPGEGEMETPSAINGNPAMHAPDSPAV 65
QY 40 D-----PLHQMPAAGDEFTFRRTFSDLAOLHTPGSAOQRFQ 81
DB 66 NCATGSSSLDAREVIMPTAVKQALREAGDEFELRYRRAFSDLTSLHTPGTAQSFQ 125
QY 82 VSDDELFOGPNMGRLVAFVFGALCAESVKNKMEPLVGVQVDMVAYLETPLADWIHS 141
DB 126 VVNELFPDGVNMGRIYAFVFGALCVESVDKEMQVLVSIAAMATYLDHLEPWIOE 185
QY 142 GGMAEFTALYGDGALBEARLRB--GNMASVTVLTGAVVALGAL 183
DB 186 GGMDFVFLVYGNMAAESRKQGERFRFRWFLTGMTVAGVLLGSL 229

RESULT 7
ID 035844 PRELIMINARY; PRT; 233 AA.
AC 035844;
DT 01-JUN-1998 (TREMBlrel. 05, Created)
DT 01-JUN-1998 (TREMBlrel. 05, Last sequence update)
DE Bcl-xL.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9350687;
RA Yang X.-F., Weber G.F., Cantor H.,
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR EMBL; U51278; AAC53459.1; -
DR HSSP; P53563; IAP3.
DR WGD; MGI:88139; Bcl2l.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM0265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26033 MW; 3083FFD8327E072E CRC64;

Query Match      43.2%; Score 435.5; DB 11; Length 233;
Best Local Similarity 41.8%; Pred. No. 1.3e-30;
Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADPVGYKLRQKGY-----V 28
DB 6 RELVVDPLSLYKLSQKGYSMQSFSDVEENRTEAPGEGEMETPSAINGNPAMHAPDSPAV 65

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QY 29 CGAGPGEPPAD-----PLHQMPAAGDEFTFRRTFSDLAOLHTPGSAOQRF 80
DB 66 NGA-TGHSSSLDAREVIMPTAVKQALREAGDEFELRYRRAFSDLTSLHTPGTAQSF 124
QY 81 QVSDDELFOGPNMGRLVAFVFGALCAESVKNKMEPLVGVQVDMVAYLETPLADWIHS 140
DB 125 QVNELFPDGVNMGRIYAFVFGALCVESVDKEMQVLVSIAAMATYLDHLEPWIOE 184
QY 141 SGMAEFTALYGDGALBEARLRB--NMASVTVLTGAVVALGAL 183
DB 185 NGMDFVFLVYGNMAAESRKQGERFRFRWFLTGMTVAGVLLGSL 229

RESULT 8
ID 08SQ42 PRELIMINARY; PRT; 233 AA.
AC 08SQ42;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Bcl-xL protein.
GN BCL-XL.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_Taxid:9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RT "Molecular cloning of feline Bcl-2 family."
RL Submitted (Mar-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB080951; BAB5856.2; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR00712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM0265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26017 MW; CD17F24F9D47BC9 CRC64;

Query Match      42.9%; Score 432.5; DB 6; Length 233;
Best Local Similarity 41.6%; Pred. No. 2.5e-30;
Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;

QY 11 RALVADPVGYKLRQKGY-----V 28
DB 6 RELVVDPLSLYKLSQKGYSMQSFSDVEENRTEAPGEGEMETPSAINGNPAMHAPDSPAV 65
QY 29 CGAGPGEPPAD-----PLHQMPAAGDEFTFRRTFSDLAOLHTPGSAOQRF 80
DB 66 NGA-TGHSSSLDAREVIMPTAVKQALREAGDEFELRYRRAFSDLTSLHTPGTAQSF 124
QY 81 QVSDDELFOGPNMGRLVAFVFGALCAESVKNKMEPLVGVQVDMVAYLETPLADWIHS 140
DB 125 QVNELFPDGVNMGRIYAFVFGALCVESVDKEMQVLVSIAAMATYLDHLEPWIOE 184
QY 141 SGMAEFTALYGDGALBEARLRB--GNMASVTVLTGAVVALGALVGAFFASK 193
DB 185 NGMDFVFLVYGNMAAESRK--QGERSNRWFLTGMTVAGVLLGSLFSRK 233

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RESULT 9  
Q9N1A2 PRELIMINARY; PRT; 233 AA.  
AC Q9N1A2; (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE Anti-apoptotic regulator Bcl-XL.  
GN BCL-XL.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
NCBI\_TaxID=9623;  
OX NCBI\_TaxID=9623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Lee T.L., Canty J.M.;  
RT "PCR Cloning of a Porcine bcl-xL cDNA from Heart";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF216205; AAF3212.1; -.  
DR HSSP; Q07817; IMAZ.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR InterPro; IPR000712; BCL2\_BH.  
DR InterPro; IPR003093; BCL2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; BCL2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;  
Query Match 42.8%; Score 431.5; DB 6; Length 233;  
Best Local Similarity 41.8%; Pred. No. 3e-30;  
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;  
QY 11 RALVADFGYKLRQGY-----V 28  
DB 6 RELVVDPLSTKLSQKGSWSQFTVEENRTAEPTGSEATPSPAINGNPSMHLADSPAV 65  
QY 29 CGAGPGGEGPAD-----PIHQAMRAAGDEFTFRFRTPSDLAQLHTVPGSAQGRFT 80  
DB 66 NGA-TGHSSSSLDAREVIMPAVAVKQALREAGDEFELRYRARSDDLTSQHLTPGTAYQSF 124  
QY 81 QVSDLEFGCGRWGRVLVAFPFPGALCAESVKNKMEPLVGVQVDMVAVYLERLADWTHS 140  
DB 125 QVVELLFRDGVNMGRIYVAFSFGALCVESVDKEMQVIVSRATWMAVYLDHLEPWIOE 184  
QY 141 SGGAAEFYALYGDGALREARLRE--GNWASVRTVLTGAVVALGAL 183  
DB 185 NGWDTFVELYGNNAAESRKQGERFRNRFMTGTVAGVLLGSL 229

RESULT 10  
Q9WZS7 PRELIMINARY; PRT; 233 AA.  
AC Q9WZS7; (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE Bcl-x long protein.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
NCBI\_TaxID=9940;  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;  
RT "Bcl-x in the sheep ovary";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF164517; AAF89532.1; -.  
DR HSSP; P53563; IAF3.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR InterPro; IPR000712; BCL2\_BH.  
DR InterPro; IPR003093; BCL2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; BCL2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;  
Query Match 42.5%; Score 428.5; DB 6; Length 233;  
Best Local Similarity 40.6%; Pred. No. 5.6e-30;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;  
QY 11 RALVADFGYKLRQGY-----VCGAGP-----GEGPAA 39  
DB 6 RELVVDPLSTKLSQKGSWSQFSDVEENRTAEPTGSDMETPSPAINGNPSMHLADSPAV 65  
QY 40 D-----PIHQAMRAAGDEFTFRFRTPSDLAQLHTVPGSAQGRFTQ 81  
DB 66 NGATGHSRSLDAREVIMPAVAVKQALREAGDEFELRYRARSDDLTSQHLTPGTAYQSF 125  
QY 82 VSDLEFGCGRWGRVLVAFPFPGALCAESVKNKMEPLVGVQVDMVAVYLERLADWTHS 141  
DB 126 VVVELLFRDGVNMGRIYVAFSFGALCVESVDKEMQVIVSRATWMAVYLDHLEPWIOE 185  
QY 142 GGMAEFTALYGDGALREARLRE--GNWASVRTVLTGAVVALGAL 183  
DB 186 GGMDTFVELYGNNAAESRKQGERFRNRFMTGTVAGVLLGSL 229

RESULT 11  
Q8BOK4 PRELIMINARY; PRT; 236 AA.  
AC Q8BOK4; (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DE B-cell leukemia/lymphoma 2.  
GN BCL2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RC MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature\_420:563-573(2002).  
 DR EMBL; AK049473; BAC33767.1; -.  
 DR MGD; MGI:88138; Bcl2.  
 DR GO; GO:0005829; C:cytosol; IDA.  
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0006915; F:apoptosis; IDA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SMO0337; BCL; 1.  
 DR SMART; SMO0265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 QO SEQUENCE 236 AA; 26437 MW; B76BFFA3A1C718 CRC64;

[illegible]

RESULT	12	
07TSN8		
ID	07TSN8	PRELIMINARY;
AC	07TSN8	PRT; 236 AA.
DT	01-OCT-2003	(TREMBLrel. 25. Created)
DT	01-OCT-2003	(TREMBLrel. 25. Last sequence update)
DT	01-OCT-2003	(TREMBLrel. 25. Last annotation update)
DE	Bcl2-like protein.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_Taxid=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Mistar;	
RA	Tanaka T.; Nangaku M.;	
RT	"Rat Bcl2-like protein."	
RL	Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.	
EMBL	AF512835; AAP47159.1; -.	
QO	SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;	

Query Match	40.8%	Score 412	DB 11	Length 226
Best Local Similarity	37.5%	Pred No. 1,6e-28		
Matches	87	Conservative 34	Mismatches 59	Indels 52
			Gaps	5
Qy	9	DTRALVADPFGYKLRQKGYVCGAG	PG	34
		10 DNRRLVMKKIHYKLRQGYEMDAGADAPLGAAPPPGTFSEOPESNPMPAVHRDWAART		69

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QY 35 -----EGPADP----LHQANRAAGDEEETRRFRTFSDLAOLHVPGSQQSFTQ 81
      |||      :      |||      |||      |||      |||      |||      |||
Db 70 SPURPLVATAGPALSPVPVVALTLRRAGDDFSRRYRRDFEAMSSQHLTLPTLRGIFAT 123
      |||      |||      |||      |||      |||      |||      |||      |||
QY 82 VSDDELFOGGNNRGLVAFVFGAALCAESVNNKEMPLVGVQODMMVAYLETRLADWTHSS 141
      |||      |||      |||      |||      |||      |||      |||      |||
Db 130 VVELLFRDGVNMRIVAAFEFGVNVCSVKNREMSPLVDNLTALMWTLEYLNHHTHWIQDN 185
      |||      |||      |||      |||      |||      |||      |||      |||
QY 142 GGAAEFATLYGGGALUEBARLREGNMWASRYTLTGAVNLGALVTVGAFFPASK 193
      |||      |||      |||      |||      |||      |||      |||      |||
Db 190 GGGDAFVELYVG---PSMRPLFDPSWLSKTLTAL--VGACITLGAYLGHK 236
      |||      |||      |||      |||      |||      |||      |||      |||

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RESULT	13		
ID	Q7TS61	PRELIMINARY;	PRT; 79 AA.
AC	Q7TS61;		
DT	01-OCT-2003 (TREMBLrel. 25, Created)		
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	BCU-Ws.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley;		
RX	MEDLINE=22672518; PubMed=12787069;		
RA	Ich T., Itch A., Pleasure D.;		
RT	"Bcl-2-related proteain family gene expression during oligodendroglial differentiation";		
RL	J. Neurochem. 85:1500-1512(2003).		
SR	EMBL; AY185099; AA064469.1; -		
SO	SEQUENCE 79 AA; 8602 MW; 47EDFB3EE2909485 CRC64;		

Query Match	40.2%	Score 406	DB 11	Length 79
Best Local Similarity	98.7%	Pred. No. 1.4e-28		
Matches 78	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	115	MEPIVGQVQDMMVATLETRLADWTHSSGGAEEFTALYGDGALBEARLRREGNWSAVRIVL	174	
Db	1	MEPIVGQVQDMMVATLETRLADWTHSSGGAEEFTALYGDGALBEARLRREGNWSAVRIVL	60	
QY	175	TGAVALGALVTVGAFPAASK	193	
Db	61	TGAVALGALVTVGAFPAASK	79	

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RESULT 14
Q9BDD5
ID Q9BDD5 PRELIMINARY; PRT; 180 AA.
AC Q9BDD5;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Anti-apoptotic regulator Bcl-xL (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eulheia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Amills M., Bouzat J.;
RL "Characterization of the bovine bcl-xL gene and related pseudogenes.",
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF245488; AAK31307.1; -
DR EMBL; AF245489; AAK31308.1; -
DR HSSP; Q07817; LMAZ.
GO GO:0016329; F:apoptosis regulator activity; IEA.
DR GO:0006915; P:apoptosis; IEA.

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DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; BCL2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS00662; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 180  
 SQ SEQUENCE 180 AA; 20062 MM; 95DC436P95DABDA6 CRC64;

Query March 39.7%; Score 401; DB 6; Length 180;  
 Best Local Similarity 53.5%; Pred. No. 1.1e-27;  
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFEFTRRRFSDLAQLHVTGSAQCRFTQVSDLELFCGPNMGRIVAFFVFG 103  
 DB 38 QALREAGDEFEFLRRRAFSDLTSQHLITPGTAYQSPQVNVNELPRDGVNMGRIVAFFSFG 97  
 QY 104 AALCAESYNKEMEPVGVQVDMVAVYETRLADWIHSSGWAFTALYGDALBEARLR 163  
 DB 98 GALTVESVDKEMQVLVSRISATWMTYLDHLEPMIOENGWDTFVELYGNNAAESRRKQ 157  
 QY 164 E-GNMA5VRTVLGAVALGAL 183  
 DB 158 ERFNRWFLTGMTVAGVLLGSL 179

RESULT 15

Q99N35 PRELIMINARY; PRT; 217 AA.  
 AC Q99N35;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE B-cell leukemia/lymphoma x (Fragment).  
 GN BCLX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RA Yang X.-F., Cantor H.;  
 RT "Novel cDNA structure and genomic organization of apoptosis regulatory  
 RT gene Bcl-x-gamma."  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF133282; AAK15455.1; -  
 DR EMBL: AF133281; AAK15455.1; JOINED.  
 DR HSSP: P53563; IAF3.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0016329; F:apoptosis regulator activity; IEA.  
 DR GO: GO:0006915; P:apoptosis; IEA.  
 DR InterPro: IPR00712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; BCL2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00662; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 180  
 SQ SEQUENCE 217 AA; 24234 MM; 3B5A4E809A7DEF18 CRC64;

Query Match 39.7%; Score 401; DB 11; Length 217;  
 Best Local Similarity 53.5%; Pred. No. 1.1e-27;  
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFEFTRRRFSDLAQLHVTGSAQCRFTQVSDLELFCGPNMGRIVAFFVFG 103

DB 72 QALREAGDEFEFLRRRAFSDLTSQHLITPGTAYQSPQVNVNELPRDGVNMGRIVAFFSFG 131  
 QY 104 AALCAESYNKEMEPVGVQVDMVAVYETRLADWIHSSGWAFTALYGDALBEARLR 163  
 DB 132 GALTVESVDKEMQVLVSRISATWMTYLDHLEPMIOENGWDTFVDLYGNNAAESRRKQ 191  
 QY 164 E-GNMA5VRTVLGAVALGAL 183  
 DB 192 ERFNRWFLTGMTVAGVLLGSL 213

Search completed: February 26, 2004, 11:14:31  
 Job time : 50 secs

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